GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 4, 2004, 11:32:18 ; Search time 14.3333 Seconds
(without alignments)
994.100 Million cell updates/sec

Title: US-10-092-404-2
Perfect score: 1520
Sequence: 1 RLLRSHSLHYLFMGASEQDL.....RYTCQVEHPGLDQPLIVIWE 276

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1520	100.0	276	4	US-09-094-964-2	Sequence 2, Appli
2	1520	100.0	348	3	US-08-652-265-6	Sequence 6, Appli
3	1520	100.0	348	3	US-08-834-497A-6	Sequence 6, Appli
4	1520	100.0	348	3	US-09-503-444A-6	Sequence 6, Appli
5	1513	99.5	276	4	US-09-094-964-1	Sequence 1, Appli
6	1513	99.5	348	3	US-08-652-265-2	Sequence 2, Appli
7	1513	99.5	348	3	US-08-834-497A-2	Sequence 2, Appli
8	1513	99.5	348	3	US-09-503-444A-2	Sequence 2, Appli
9	1513	99.5	348	4	US-09-277-457-2	Sequence 2, Appli
10	1513	99.5	348	4	US-09-679-729-2	Sequence 2, Appli
11	1509	99.3	348	3	US-08-652-265-8	Sequence 8, Appli
12	1509	99.3	348	3	US-08-834-497A-8	Sequence 8, Appli
13	1509	99.3	348	3	US-09-503-444A-8	Sequence 8, Appli
14	1502	98.8	348	3	US-08-652-265-4	Sequence 4, Appli
15	1502	98.8	348	3	US-08-834-497A-4	Sequence 4, Appli
16	1502	98.8	348	3	US-09-503-444A-4	Sequence 4, Appli
17	1493	98.2	276	4	US-09-094-964-3	Sequence 3, Appli
18	523	34.4	361	3	US-08-652-265-22	Sequence 22, Appl
19	523	34.4	361	3	US-08-834-497A-22	Sequence 22, Appl
20	523	34.4	361	3	US-09-503-444A-22	Sequence 22, Appl
21	517	34.0	364	4	US-08-914-372C-11	Sequence 11, Appl
22	514	33.8	365	3	US-08-652-265-23	Sequence 23, Appl
23	514	33.8	365	3	US-08-834-497A-23	Sequence 23, Appl
24	514	33.8	365	3	US-09-503-444A-23	Sequence 23, Appl
25	506	33.3	274	2	US-08-484-905-107	Sequence 107, App
26	506	33.3	274	3	US-08-481-985B-107	Sequence 107, App
27	506	33.3	274	3	US-08-370-476-107	Sequence 107, App
28	506	33.3	341	3	US-08-890-719-38	Sequence 38, Appl
29	505	33.2	365	2	US-08-484-905-97	Sequence 97, Appl
30	505	33.2	365	3	US-08-481-985B-97	Sequence 97, Appl
31	505	33.2	365	3	US-08-370-476-97	Sequence 97, Appl
32	504	33.2	274	2	US-08-484-905-108	Sequence 108, App
33	504	33.2	274	3	US-08-481-985B-108	Sequence 108, App
34	504	33.2	274	3	US-08-370-476-108	Sequence 108, App
35	504	33.2	365	2	US-08-484-905-100	Sequence 100, App
36	504	33.2	365	3	US-08-481-985B-100	Sequence 100, App
37	504	33.2	365	3	US-08-370-476-100	Sequence 100, App
38	503	33.1	274	1	US-08-222-851-1	Sequence 1, Appli
39	503	33.1	363	4	US-08-914-372C-37	Sequence 37, Appl
40	503	33.1	365	2	US-08-484-905-99	Sequence 99, Appl
41	503	33.1	365	3	US-08-481-985B-99	Sequence 99, Appl
42	503	33.1	365	3	US-08-370-476-99	Sequence 99, Appl
43	502	33.0	274	2	US-08-484-905-106	Sequence 106, App
44	502	33.0	274	3	US-08-481-985B-106	Sequence 106, App
45	502	33.0	274	3	US-08-370-476-106	Sequence 106, App

ALIGNMENTS

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RESULT 1
US-09-094-964-2
; Sequence 2, Application US/09094964
; Patent No. 6391852
;  GENERAL INFORMATION:
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Bjorkman, Pamela J.
;    APPLICANT:  Schatzman, Randall C.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF IRON OVERLOAD DISEASES
;    TITLE OF INVENTION:  AND IRON DEFICIENCY DISEASES
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds, LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/094,964
;      FILING DATE:  June 12, 1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/876,010
;      FILING DATE:  June 13, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0074-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  276 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-094-964-2

  Query Match            100.0%;  Score 1520;  DB 4;  Length 276;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-142;
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  Matches  276;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
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Db          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
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Db        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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RESULT 2
US-08-652-265-6
; Sequence 6, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-265-6

  Query Match           100.0%;  Score 1520;  DB 3;  Length 348;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-142;
  Matches  276;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
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Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
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Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
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Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 3
US-08-834-497A-6
; Sequence 6, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  B907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
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;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/094,964
;            FILING DATE: June 12, 1998
;            APPLICATION NUMBER: 08/876,010
;            FILING DATE: June 13, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Poissant, Brian M
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-0074-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650-493-4935
;            TELEFAX: 650-493-5556
;            TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 276 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-092-404-1

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  Best Local Similarity   99.6%;  Pred. No. 4.5e-145;
  Matches  275;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
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Db         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
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Db        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
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Db        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276


RESULT 4
US-09-981-606-2
; Sequence 2, Application US/09981606
; Publication No. US20030129595A1
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg et al.
;  TITLE OF INVENTION: Mutations associated with iron disorders
;  FILE REFERENCE: 24065-004CON
;  CURRENT APPLICATION NUMBER: US/09/981,606
;  CURRENT FILING DATE:  2002-10-16
;  PRIOR APPLICATION NUMBER: 09/277,457
;  PRIOR FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 348
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-981-606-2

  Query Match             99.5%;  Score 1513;  DB 10;  Length 348;
  Best Local Similarity   99.6%;  Pred. No. 6.2e-145;
  Matches  275;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
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Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
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Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 5
US-10-138-888-2
; Sequence 2, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 348 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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US-10-138-888-2

Query Match 99.5%; Score 1513; DB 14; Length 348;
Best Local Similarity 99.6%; Pred. No. 6.2e-145;
Matches 275; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
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Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298
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RESULT 6
US-10-138-888-8
; Sequence 8, Application US/10138888
; Publication No. US20030148972A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; Drayna, Dennis T.
; Feder, John N.
; Gnirke, Andreas
; Ruddy, David
; Tsuchihashi, Zenta
; Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/138,888
; FILING DATE: 02-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/834,497
; FILING DATE: 04-APR-1997
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brian M. Poissant
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-095-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864

; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-138-888-8

Query Match 99.3%; Score 1509; DB 14; Length 348;
Best Local Similarity 99.6%; Pred. No. 1.6e-144;
Matches 275; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||| ||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTYQVEHPGLDQPLIVIWE 298
```

RESULT 7
US-10-138-888-78
; Sequence 78, Application US/10138888
; Publication No. US20030148972A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; Drayna, Dennis T.
; Feder, John N.
; Gnirke, Andreas
; Ruddy, David
; Tsuchihashi, Zenta
; Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/138,888
; FILING DATE: 02-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/834,497
; FILING DATE: 04-APR-1997
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996

```
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 78:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 348 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-10-138-888-78

  Query Match             99.2%;  Score 1508;  DB 14;  Length 348;
  Best Local Similarity   99.3%;  Pred. No. 2e-144;
  Matches  274;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              |||||||||||||||||||||||||||||||||||||||| | ||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHECRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 8
US-10-138-888-4
; Sequence 4, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 348 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-138-888-4

  Query Match             98.8%;  Score 1502;  DB 14;  Length 348;
  Best Local Similarity   99.3%;  Pred. No. 8.1e-144;
  Matches  274;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||| ||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTYQVEHPGLDQPLIVIWE 298


RESULT 9
US-10-092-404-3
; Sequence 3, Application US/10092404
; Publication No. US20030073627A1
;   GENERAL INFORMATION:
;       APPLICANT: Feder, John N.
;                  Bjorkman, Pamela J.
;                  Schatzman, Randall C.
;       TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
;                           DIAGNOSIS AND TREATMENT OF IRON OVERLOAD DISEASES
;                           AND IRON DEFICIENCY DISEASES
;       NUMBER OF SEQUENCES: 5
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds, LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036-2811
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows
;            SOFTWARE: FastSEQ for Windows Version 2.0b
;       CURRENT APPLICATION DATA:
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;             APPLICATION NUMBER: US/10/092,404
;             FILING DATE: 04-Mar-2002
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/094,964
;             FILING DATE: June 12, 1998
;             APPLICATION NUMBER: 08/876,010
;             FILING DATE: June 13, 1997
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Poissant, Brian M
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-0074-999
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
;             TELEFAX: 650-493-5556
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 276 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-092-404-3

  Query Match             98.2%;  Score 1493;  DB 14;  Length 276;
  Best Local Similarity   98.9%;  Pred. No. 4.9e-143;
  Matches  273;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276


RESULT 10
US-10-143-822-1
; Sequence 1, Application US/10143822
; Publication No. US20030215808A1
; GENERAL INFORMATION:
;  APPLICANT: Institut National de la Sante et de la Recherche Medicale
;  APPLICANT:  Institut Curie
;  TITLE OF INVENTION: A T cell subpopulation regulating gut immunity
;  FILE REFERENCE: BO133US
;  CURRENT APPLICATION NUMBER: US/10/143,822
;  CURRENT FILING DATE:  2002-05-14
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 341
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-143-822-1

  Query Match             35.7%;  Score 542.5;  DB 15;  Length 341;
  Best Local Similarity   39.5%;  Pred. No. 2.2e-46;
  Matches  107;  Conservative   50;  Mismatches  111;  Indels    3;  Gaps    3;

Qy          4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQMWL 63
              |:||| |  :| |:   |:  | ::|||| ||  :|: ||| ||::  ::   |
Db         23 RTHSLRYFRLGVSDPIHGVPEFISVGYVDSHPITTYDSVTRQKEPRAPWMAENLAPDHWE 82

Qy         64 QLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDH 123
              : :| |:||  || |:   :  ::||| ||| | ::|||: || || |: : | |||||
Db         83 RYTQLLRGWQQMFKVELKRLQRHYNHS-GSHTYQRMIGCELLEDGSTTGFLQYAYDGQDF 141

Qy        124 LEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQ 183
              | |  ||| | | :  |   | || ::     : :|| :| | |:: || |:  | :
Db        142 LIFNKDTLSWLAVDNVAHTIKQAWEANQHELLYQKNWLEEECIAWLKRFLEYGKDTLQRT 201

Qy        184 VPPLVKVTHHVT-SSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTY 242
              ||||:|   |  || | |:|  :||  | | |:|: : :  :| :  |:||:|||||
Db        202 EPPLVRVNRKETFPGVTALFCKAHGFYPPEIYMTWMKNGEEI-VQEIDYGDILPSGDGTY 260

Qy        243 QGWITLAVPPGEEQRYTCQVEHPGLDQPLIV 273
              | | :: : |    |:| ||| |:   | |
Db        261 QAWASIELDPQSSNLYSCHVEHCGVHMVLQV 291


RESULT 11
US-10-138-888-22
; Sequence 22, Application US/10138888
; Publication No. US20030148972A1
;   GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;   INFORMATION FOR SEQ ID NO: 22:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 361 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
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;           TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         FEATURE:
;              NAME/KEY:  Protein
;              LOCATION:  1..361
;              OTHER INFORMATION:  /note= "Rabbit leukocyte antigen (RLA)"
;         SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-138-888-22

  Query Match             34.4%;  Score 523;  DB 14;  Length 361;
  Best Local Similarity   40.1%;  Pred. No. 2.3e-44;
  Matches  111;  Conservative   44;  Mismatches  114;  Indels    8;  Gaps    7;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDE--SRRVEPRTPWVSSRISSQMW 62
              |||: | :   |   ||   |  :|||||  || :| :  | |:| | ||:  ::  : |
Db         26 SHSMRYFYTSVSRPGLGEPRFIIVGYVDDTQFVRFDSDAASPRMEQRAPWM-GQVEPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNHSKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
              | :|  |     | |:  | :  :| |   ||| | : |||:  |     || :| |||
Db         85 DQQTQIAKDTAQTFRVNLNTALRYYNQSAAGSHTFQTMFGCEVWADGRFFHGYRQYAYDG 144

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              |::     |  | ||:  |  |: :||     | ::|||||:|   |:: ||:|:  |
Db        145 ADYIALNEDLRSWTAADTAAQNTQRKWEAAG-EAERHRAYLERECVEWLRRYLEMGKETL 203

Qy        181 DQQVPPLVKVTHHVTSS-VTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :  ||   |||| |    |||| || :||  |:: | :| :    :: |  :  | ||
Db        204 QRADPPKAHVTHHPASDREATLRCWALGFYPAEISLTWQRDGED-QTQDTELVETRPGGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |||||||||:|:| || :|| : ||
Db        263 GTFQKWAAVVVPSGEEQRYTCRVQHEGLPEPLTLTWE 299


RESULT 12
US-10-016-634A-120
; Sequence 120, Application US/10016634A
; Publication No. US20020192666A1
; GENERAL INFORMATION:
;  APPLICANT: Sun, Yongming
;  APPLICANT:  Recipon, Herve
;  APPLICANT:  Ghosh, Malavika
;  APPLICANT:  Liu, Chenghua
;  TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Prc
;  FILE REFERENCE: DEX-0255
;  CURRENT APPLICATION NUMBER: US/10/016,634A
;  CURRENT FILING DATE:  2001-10-31
;  PRIOR APPLICATION NUMBER: US 60/244,258
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 176
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
;   LENGTH: 92
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-016-634A-120

  Query Match             33.8%;  Score 514;  DB 13;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-44;
  Matches   92;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         92 ESHTLQVILGCEMQEDNSTEGYWKYGYDGQDHLEFCPDTLDWRAAEPRAWPTKLEWERHK 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ESHTLQVILGCEMQEDNSTEGYWKYGYDGQDHLEFCPDTLDWRAAEPRAWPTKLEWERHK 60

Qy        152 IRARQNRAYLERDCPAQLQQLLELGRGVLDQQ 183
              ||||||||||||||||||||||||||||||||
Db         61 IRARQNRAYLERDCPAQLQQLLELGRGVLDQQ 92


RESULT 13
US-10-138-888-23
; Sequence 23, Application US/10138888
; Publication No. US20030148972A1
;  GENERAL INFORMATION:
;       APPLICANT: Thomas, Winston J.
;                  Drayna, Dennis T.
;                  Feder, John N.
;                  Gnirke, Andreas
;                  Ruddy, David
;                  Tsuchihashi, Zenta
;                  Wolff, Roger K.
;       TITLE OF INVENTION: Hereditary Hemochromatosis Gene
;       NUMBER OF SEQUENCES: 79
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/138,888
;            FILING DATE: 02-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/834,497
;            FILING DATE: 04-APR-1997
;            APPLICATION NUMBER: US 08/652,265
;            FILING DATE: 23-MAY-1996
;            APPLICATION NUMBER: US 08/632,673
;            FILING DATE: 16-APR-1996
;            APPLICATION NUMBER: US 08/630,912
;            FILING DATE: 04-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brian M. Poissant
;            REGISTRATION NUMBER: 28,462
;            REFERENCE/DOCKET NUMBER: 8907-095-999
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-8864
;  INFORMATION FOR SEQ ID NO: 23:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 365 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       FEATURE:
;            NAME/KEY:  Protein
;            LOCATION:  1..365
;            OTHER INFORMATION:  /note= "Human Major Histocompatability
;            Class I (MHC) protein"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-138-888-23

  Query Match             33.8%;  Score 514;  DB 14;  Length 365;
  Best Local Similarity   39.7%;  Pred. No. 1.9e-43;
  Matches  110;  Conservative   45;  Mismatches  114;  Indels    8;  Gaps    7;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |     |   | |:|||||  || :| :  |:|:||| ||:      : |
Db         26 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNHSKE-SHTLQVILGCEMQED-NSTEGYWKYGYDG 120
                :: :|        ||  |:   :| |:  |||||:: ||::  |      || :| |||
Db         85 DGETRKVKAHSQTHRVDLGTLRGYYNQSEAGSHTLQMMFGCDVGSDWRFLRGYHQYAYDG 144

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :|::    |   | ||:  |  || :||   : | | |||||  |   |:: || |:  |
Db        145 KDYIALKEDLRSWTAADMAAQTTKHKWEAAHV-AEQLRAYLEGTCVEWLRRYLENGKETL 203
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Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :   |   :||| |:    ||||  ||::||  ||: | :| :    :: |  :  | ||
Db        204 QRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGED-QTQDTELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |:|||||| |:| || :|| : ||
Db        263 GTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRWE 299


RESULT 14
US-10-073-300-6
; Sequence 6, Application US/10073300
; Publication No. US20030003535A1
; GENERAL INFORMATION:
;  APPLICANT: Reiter, Yoram
;  TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
;  FILE REFERENCE: 02/23339
;  CURRENT APPLICATION NUMBER: US/10/073,300
;  CURRENT FILING DATE:  2002-06-25
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 280
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-073-300-6

  Query Match             33.3%;  Score 506;  DB 14;  Length 280;
  Best Local Similarity   39.4%;  Pred. No. 8.8e-43;
  Matches  109;  Conservative   45;  Mismatches  115;  Indels    8;  Gaps    7;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |    |   | |:|||||  || :| :  |:|:|:|| ||:      : |
Db          2 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 60

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNHSKE-SHTLQVILGCEMQED-NSTEGYWKYGYDG 120
                :: :|       ||  |:   :| |:  |||:| : ||::  |     || :| |||
Db         61 DGETRKVKAHSQTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDVGSDWRFLRGYHQYAYDG 120

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :|::    |   | ||:  |  || :||   : | | |||||  |   |:: || |:  |
Db        121 KDYIALKEDLRSWTAADMAAQTTKHKWEAAHV-AEQLRAYLEGTCVEWLRRYLENGKETL 179

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :   |   :||| |:    ||||  ||::||  ||: | :| :    :: |  :  | ||
Db        180 QRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGED-QTQDTELVETRPAGD 238

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |:|||||| |:| || :|| : ||
Db        239 GTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRWE 275


RESULT 15
US-10-073-300-5
; Sequence 5, Application US/10073300
; Publication No. US20030003535A1
; GENERAL INFORMATION:
;  APPLICANT: Reiter, Yoram
;  TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
;  FILE REFERENCE: 02/23339
;  CURRENT APPLICATION NUMBER: US/10/073,300
;  CURRENT FILING DATE:  2002-06-25
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 415
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: human beta2 microglobulin linked to MHC class I heavy chain
US-10-073-300-5

  Query Match             33.3%;  Score 506;  DB 14;  Length 415;
  Best Local Similarity   39.4%;  Pred. No. 1.5e-42;
  Matches  109;  Conservative   45;  Mismatches  115;  Indels    8;  Gaps    7;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |    |   | |:|||||  || :| :  |:|:|:|| ||:      : |
Db        117 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 175

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNHSKE-SHTLQVILGCEMQED-NSTEGYWKYGYDG 120
                :: :|       ||  |:   :| |:  |||:| : ||::  |     || :| |||
Db        176 DGETRKVKAHSQTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDVGSDWRFLRGYHQYAYDG 235

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :|::    |   | ||:  |  || :||   : | | |||||  |   |:: || |:  |
Db        236 KDYIALKEDLRSWTAADMAAQTTKHKWEAAHV-AEQLRAYLEGTCVEWLRRYLENGKETL 294

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :   |   :||| |:    ||||  ||::||  ||: | :| :    :: |  :  | ||
Db        295 QRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGED-QTQDTELVETRPAGD 353

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |:|||||| |:| || :|| : ||
Db        354 GTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRWE 390


Search completed: May  4, 2004, 11:50:58
Job time : 37 secs
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;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-834-497A-6

  Query Match             100.0%;  Score 1520;  DB 3;  Length 348;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-142;
  Matches  276;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 4
US-09-503-444A-6
; Sequence 6, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-503-444A-6

  Query Match             100.0%;  Score 1520;  DB 3;  Length 348;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-142;
  Matches  276;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 5
US-09-094-964-1
; Sequence 1, Application US/09094964
; Patent No. 6391852
;  GENERAL INFORMATION:
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Bjorkman, Pamela J.
;    APPLICANT:  Schatzman, Randall C.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF IRON OVERLOAD DISEASES
;    TITLE OF INVENTION:  AND IRON DEFICIENCY DISEASES
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds, LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/094,964
;      FILING DATE:  June 12, 1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/876,010
;      FILING DATE:  June 13, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0074-999
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  276 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-094-964-1

  Query Match             99.5%;  Score 1513;  DB 4;  Length 276;
  Best Local Similarity   99.6%;  Pred. No. 1.4e-141;
  Matches  275;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276


RESULT 6
US-08-652-265-2
; Sequence 2, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-265-2

  Query Match             99.5%;  Score 1513;  DB 3;  Length 348;
  Best Local Similarity   99.6%;  Pred. No. 1.9e-141;
  Matches  275;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 7
US-08-834-497A-2
; Sequence 2, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-834-497A-2

  Query Match             99.5%;  Score 1513;  DB 3;  Length 348;
  Best Local Similarity   99.6%;  Pred. No. 1.9e-141;
  Matches  275;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 8
US-09-503-444A-2
; Sequence 2, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-503-444A-2

  Query Match             99.5%;  Score 1513;  DB 3;  Length 348;
  Best Local Similarity   99.6%;  Pred. No. 1.9e-141;
  Matches  275;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 9
US-09-277-457-2
; Sequence 2, Application US/09277457
; Patent No. 6355425
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg, Barry E.
;  APPLICANT:  Sawada-Hirai, Ritsuko
;  APPLICANT:  Barton, James C.
;  TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
;  FILE REFERENCE: 10653/002001
;  CURRENT APPLICATION NUMBER: US/09/277,457
;  CURRENT FILING DATE:  1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 348
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-277-457-2

  Query Match             99.5%;  Score 1513;  DB 4;  Length 348;
  Best Local Similarity   99.6%;  Pred. No. 1.9e-141;
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  Matches  275;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 10
US-09-679-729-2
; Sequence 2, Application US/09679729
; Patent No. 6509442
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg, Barry E.
;  APPLICANT:  Sawada-Hirai, Ritsuko
;  APPLICANT:  Barton, James C.
;  TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
;  FILE REFERENCE: 24065-004 DIV
;  CURRENT APPLICATION NUMBER: US/09/679,729
;  CURRENT FILING DATE:  2000-10-04
;  PRIOR APPLICATION NUMBER: 09/277,457
;  PRIOR FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 348
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-679-729-2

  Query Match             99.5%;  Score 1513;  DB 4;  Length 348;
  Best Local Similarity   99.6%;  Pred. No. 1.9e-141;
  Matches  275;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 11
US-08-652-265-8
; Sequence 8, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-265-8

  Query Match             99.3%;  Score 1509;  DB 3;  Length 348;
  Best Local Similarity   99.6%;  Pred. No. 4.8e-141;
  Matches  275;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        263 TYQGWITLAVPPGEEQRYTYQVEHPGLDQPLIVIWE 298


RESULT 12
US-08-834-497A-8
; Sequence 8, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
```

```
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-834-497A-8

  Query Match             99.3%;  Score 1509;  DB 3;  Length 348;
  Best Local Similarity   99.6%;  Pred. No. 4.8e-141;
  Matches  275;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||||||||||||||||||| ||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTYQVEHPGLDQPLIVIWE 298


RESULT 13
US-09-503-444A-8
; Sequence 8, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-503-444A-8

  Query Match             99.3%;  Score 1509;  DB 3;  Length 348;
  Best Local Similarity   99.6%;  Pred. No. 4.8e-141;
  Matches  275;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        263 TYQGWITLAVPPGEEQRYTYQVEHPGLDQPLIVIWE 298


RESULT 14
US-08-652-265-4
; Sequence 4, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-265-4

  Query Match             98.8%;  Score 1502;  DB 3;  Length 348;
  Best Local Similarity   99.3%;  Pred. No. 2.3e-140;
  Matches  274;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||| ||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTYQVEHPGLDQPLIVIWE 298


RESULT 15
US-08-834-497A-4
; Sequence 4, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-834-497A-4

  Query Match             98.8%;  Score 1502;  DB 3;  Length 348;
  Best Local Similarity   99.3%;  Pred. No. 2.3e-140;
  Matches  274;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82
```

```
Qy          61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy         121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy         181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy         241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
               |||||||||||||||| ||||||||||||||||
Db         263 TYQGWITLAVPPGEEQRYTYQVEHPGLDQPLIVIWE 298
```

Search completed: May 4, 2004, 11:36:35
Job time : 14.3333 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 4, 2004, 11:32:18 ; Search time 13.6667 Seconds
(without alignments)
1942.600 Million cell updates/sec

Title: US-10-092-404-3
Perfect score: 1514
Sequence: 1 RLLRSHSLHYLFMGASEQDL.....RYTCQVEHPGLDQPLIVIWE 276

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1129	74.6	359	2	JC5382	hereditary hemochr
2	530.5	35.0	341	2	A57136	class I histocompa
3	517	34.1	361	1	HLRB	MHC class I histoc
4	517	34.1	361	2	I46858	MHC class I RLA pr
5	514	33.9	332	2	S06424	MHC class I histoc
6	511	33.8	365	2	I36961	MHC class I protei
7	510	33.7	361	2	B27638	MHC class I histoc
8	509	33.6	365	2	I83063	A11.2 - human
9	508	33.6	365	2	A47636	MHC class I histoc
10	508	33.6	365	2	I56039	HLA-A30.3 precurso
11	506	33.4	370	1	HLHUA3	MHC class I histoc
12	504	33.3	365	2	I38439	MHC class I histoc
13	503	33.2	365	2	I37542	MHC class I histoc
14	503	33.2	365	2	I38442	gene HLA-A-0205 pr
15	503	33.2	365	2	I61902	MHC class I histoc
16	502	33.2	365	2	I72170	MHC class I histoc
17	502	33.2	365	2	I38441	gene HLA-A-6802 pr
18	501	33.1	355	2	T28149	MHC class I histoc
19	500	33.0	365	1	HLHUA2	MHC class I histoc
20	500	33.0	365	2	I37482	MHC class I histoc
21	500	33.0	365	2	I38519	MHC class I histoc
22	500	33.0	365	2	I84448	MHC class I histoc
23	499	33.0	365	2	I38610	MHC class I histoc
24	499	33.0	365	2	I37470	HLA-A*0210 - human
25	498	32.9	364	2	S03535	class I histocompa
26	497	32.8	365	2	I37476	MHC class I histoc
27	497	32.8	365	2	I37478	MHC class I histoc
28	497	32.8	365	2	I38443	gene HLA-A-0203 pr
29	497	32.8	365	2	I61857	MHC HLA-A2.4a chai
30	496	32.8	357	2	I36965	MHC class I protei
31	495.5	32.7	362	2	A45845	MHC class I histoc
32	495	32.7	365	2	I61856	MHC class I histoc
33	495	32.7	365	2	I54493	MHC class I histoc
34	494	32.6	273	1	HLHU69	MHC class I histoc
35	494	32.6	279	2	JX0353	zinc-alpha 2-glyco
36	494	32.6	365	2	S77963	MHC class I histoc
37	494	32.6	365	2	S01171	class I histocompa
38	494	32.6	365	2	I54416	HLA-AW24 protein -
39	493	32.6	365	2	I37483	HLA-Aw34.2 antigen
40	492	32.5	273	1	HLHUAW	MHC class I histoc
41	492	32.5	360	2	A27638	MHC class I histoc
42	492	32.5	365	2	I72171	HLA-Aw33.1, HLA-Aw
43	491.5	32.5	339	2	I56071	MHC class I histoc
44	491	32.4	362	2	I68724	MHC class I histoc
45	490.5	32.4	341	2	JC5663	major histocompati

ALIGNMENTS

RESULT 1
JC5382
hereditary hemochromatosis protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 05-Nov-1999
C;Accession: JC5382
R;Hashimoto, K.; Hirai, M.; Kurosawa, Y.
Biochem. Biophys. Res. Commun. 230, 35-39, 1997
A;Title: Identification of a mouse homolog for the human hereditary haemochromatosis ca
A;Reference number: JC5382; MUID:97148566; PMID:9020055
A;Accession: JC5382
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-359 <HAS>
A;Cross-references: GB:U66849; NID:g1519484; PIDN:AAB07525.1; PID:g1519485
C;Comment: This protein plays a role in iron metabolism.
C;Genetics:
A;Gene: mr2
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-359/Product: hereditary haemochromatosis protein #status predicted <MAT>
F;30-117/Domain: alpha 1 #status predicted <ALF1>
F;118-217/Domain: alpha 2 #status predicted <ALF2>
F;218-309/Domain: alpha 3 #status predicted <ALF3>
F;314-340/Domain: transmembrane #status predicted <TRM>
F;341-359/Domain: intracellular #status predicted <INT>

Query Match 74.6%; Score 1129; DB 2; Length 359;
Best Local Similarity 71.9%; Pred. No. 1.8e-86;
Matches 202; Conservative 30; Mismatches 41; Indels 8; Gaps 1;

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Qy          4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWL 63
              ||||| |||||||| |||| |||| ||||||||| |:||||| ||| ||:  : |||:||
Db         30 RSHSLRYLFMGASEPDLGLPLFEARGYVDDQLFVSYNHESRRAEPRAPWILEQTSSQLWL 89

Qy         64 QLSQSLKGWDHMFTVDFWTIMENHNASK--------ESHTLQVILGCEMQEDNSTEGYWK 115
               |||||||||:|| |||||| |:| ||         ||| |||:|||| ||||| |:|:
Db         90 HLSQSLKGWDYMFIVDFWTIMGNYNHSKVTKLGVVSESHILQVVLGCEVHEDNSTSGFWR 149

Qy        116 YGYDGQDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLEL 175
              ||||||| ||||| ||:| |||| || ||:||: |||||:||| |||:||| ||::||||
Db        150 YGYDGQDHLEFCPKTLNWSAAEPGAWATKVEWDEHKIRAKQNRDYLEKDCPEQLKRLLEL 209

Qy        176 GRGVLDQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVL 235
              ||||| |||| ||||| |  |: |:|||:||:::||||||:|||| ||:|||:  |: ||
Db        210 GRGVLGQQVPTLVKVTRHWASTGTSLRCQALDFFPQNITMRWLKDNQPLDAKDVNPEKVL 269

Qy        236 PNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||| |||||:|||| ||:| |:||||||||||||||   ||
Db        270 PNGDETYQGWLTLAVAPGDETRFTCQVEHPGLDQPLTASWE 310
```

RESULT 2
A57136
class I histocompatibility antigen related protein MR1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Jul-1999
C;Accession: A57136
R;Hashimoto, K.; Hirai, M.; Kurosawa, Y.
Science 269, 693-695, 1995
A;Title: A gene outside the human MHC related to classical HLA class I genes.
A;Reference number: A57136; MUID:95350662; PMID:7624800
A;Accession: A57136
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-341 <HAS>
A;Cross-references: GB:U22963; NID:g940353; PIDN:AAC50174.1; PID:g940354
C;Genetics:
A;Gene: GDB:HLALS
A;Cross-references: GDB:683188; OMIM:600764
A;Map position: 1q25.3-1q25.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 35.0%; Score 530.5; DB 2; Length 341;
Best Local Similarity 39.1%; Pred. No. 1.2e-36;
Matches 106; Conservative 50; Mismatches 112; Indels 3; Gaps 3;

```
Qy          4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWL 63
              |:||| |  :| |:   |:  | ::||||      ||  :|: ||| ||::  ::   |
Db         23 RTHSLRYFRLGVSDPIHGVPEFISVGYVDSHPITTYDSVTRQKEPRAPWMAENLAPDHWE 82

Qy         64 QLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDA 123
              : :| |:||  || |:   :  ::| |  ||| | ::|||: || || |: :| |||||
Db         83 RYTQLLRGWQQMFKVELKRLQRHYNHS-GSHTYQRMIGCELLEDGSTTGFLQYAYDGQDF 141

Qy        124 LEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQ 183
              | |  ||| | |  :   |  || ::      : :|| :| | |:: || |:  | :
Db        142 LIFNKDTLSWLAVDNVAHTIKQAWEANQHELLYQKNWLEEECIAWLKRFLEYGKDTLQRT 201

Qy        184 VPPLVKVTHHVT-SSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTY 242
              ||||:|   |   || | |:|  :||  | | |:|: : :  :| :  |:||:|||||
Db        202 EPPLVRVNRKETFPGVTALFCKAHGFYPPEIYMTWMKNGEEI-VQEIDYGDILPSGDGTY 260

Qy        243 QGWITLAVPPGEEQRYTCQVEHPGLDQPLIV 273
              | | :: : |     |:| ||| |:   | |
Db        261 QAWASIELDPQSSNLYSCHVEHCGVHMVLQV 291
```

RESULT 3
HLRB
MHC class I histocompatibility antigen RLA alpha chain precursor (RL-5) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 22-Jun-1999
C;Accession: A02193
R;Tykocinski, M.L.; Marche, P.N.; Max, E.E.; Kindt, T.J.
J. Immunol. 133, 2261-2269, 1984
A;Title: Rabbit class I MHC genes: cDNA clones define full-length transcripts of an expr
A;Reference number: A02193; MUID:84290724; PMID:6432910
A;Accession: A02193
A;Molecule type: mRNA
A;Residues: 1-361 <TYK>
A;Cross-references: GB:K02441; NID:g1293894; PIDN:AAA98729.1; PID:g165496
A;Note: the source of this protein is a T-lymphoid cell line (RL-5), which has been tran
C;Comment: In contrast to the many antigens expressed in mouse (K, D, and L) and human (
MHC may therefore differ from the HLA and H-2 loci in having limited complexity.
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterodimer; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-361/Product: class I histocompatibility antigen RLA alpha chain #status predicted <
F;25-307/Domain: extracellular #status predicted <EXT>
F;25-114/Domain: alpha-1 <EX1>
F;115-206/Domain: alpha-2 <EX2>
F;220-285/Domain: immunoglobulin homology <IMM>
F;308-329/Domain: transmembrane #status predicted <TMM>
F;330-361/Domain: intracellular #status predicted <INT>
F;110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;125-188,227-283/Disulfide bonds: #status predicted

Query Match 34.1%; Score 517; DB 1; Length 361;
Best Local Similarity 40.1%; Pred. No. 1.7e-35;
Matches 111; Conservative 43; Mismatches 115; Indels 8; Gaps 7;

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Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | :   |   ||   |  :|||||  || :| :  | |:| | ||:  ::  : |
Db         26 SHSMRYFYTSVSRPGLGEPRFIIVGYVDDTQFVRFDSDAASPRMEQRAPWM-GQVEPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
              | :|  |     | |:  | :  :| |  ||| | : |||:  |    || :| |||
Db         85 DQQTQIAKDTAQTFRVNLNTALRYYNQSAAGSHTFQTMFGCEVWADGRFFHGYRQYAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              | :    |   | ||:  |  |: :||     | ::|||||:|   |:: ||:|:  |
Db        145 ADYIALNEDLRSWTAADTAAQNTQRKWEAAG-EAERHRAYLERECVEWLRRYLEMGKETL 203

Qy        181 DQQVPPLVKVTHHVTSS-VTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :  ||   |||  |    |||| || :||  |:: | :| :    :: |  :  | ||
Db        204 QRADPPKAHVTHHPASDREATLRCWALGFYPAEISLTWQRDGED-QTQDTELVETRPGGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || ||||||||:|:| || :|| : ||
Db        263 GTFQKWAAVVVPSGEEQRYTCRVQHEGLPEPLTLTWE 299
```

RESULT 4
I46858
MHC class I RLA precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 21-Jan-2000
C;Accession: I46858
R;Marche, P.N.; Tykocinski, M.L.; Max, E.E.; Kindt, T.J.
Immunogenetics 21, 71-82, 1985
A;Title: Structure of a functional rabbit class I MHC gene: Similarity to human class I
A;Reference number: I46858; MUID:85103547; PMID:3917974
A;Accession: I46858
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-361 <MAR>
A;Cross-references: GB:K02819; NID:g165497; PIDN:AAA98730.1; PID:g165498
C;Genetics:
A;Introns: 25/1; 115/1; 207/1; 299/1; 337/1; 348/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 34.1%; Score 517; DB 2; Length 361;
Best Local Similarity 40.1%; Pred. No. 1.7e-35;
Matches 111; Conservative 43; Mismatches 115; Indels 8; Gaps 7;

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Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | :   |   ||   |  :|||||  || :| :  | |:| | ||:  ::  : |
Db         26 SHSMRYFYTSVSRPGLGEPRFIIVGYVDDTQFVRFDSDAASPRMEQRAPWM-GQVEPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
              | :|  |     | |:  | :  :| |  ||| | : |||:  |    || :| |||
Db         85 DQQTQIAKDTAQTFRVNLNTALRYYNQSAAGSHTFQTMFGCEVWADGRFFHGYRQYAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              | :    |   | ||:  |  |: :||     | ::|||||:|   |:: ||:|:  |
Db        145 ADYIALNEDLRSWTAADTAAQNTQRKWEAAG-EAERHRAYLERECVEWLRRYLEMGKETL 203

Qy        181 DQQVPPLVKVTHHVTSS-VTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :  ||   |||  |    |||| || :||  |:: | :| :    :: |  :  | ||
Db        204 QRADPPKAHVTHHPASDREATLRCWALGFYPAEISLTWQRDGED-QTQDTELVETRPGGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || ||||||||:|:| || :|| : ||
Db        263 GTFQKWAAVVVPSGEEQRYTCRVQHEGLPEPLTLTWE 299
```

RESULT 5
S06424
MHC class I histocompatibility antigen Ch25 alpha chain precursor - chimpanzee
N;Alternate names: MHC ChlA chain
C;Species: Pan troglodytes (chimpanzee)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 23-Jul-1999
C;Accession: S06424; I36959
R;Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.
Nature 335, 268-271, 1988
A;Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.
A;Reference number: S06424; MUID:88319000; PMID:3412487
A;Accession: S06424
A;Molecule type: mRNA
A;Residues: 1-332 <LAW>
R;Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A;Title: Diversity and diversification of HLA-A,B,C alleles.
A;Reference number: I36956; MUID:89235215; PMID:2715640
A;Accession: I36959
A;Molecule type: mRNA
A;Residues: 1-332 <RES>
A;Cross-references: GB:M24047; NID:g176818; PIDN:AAA35426.1; PID:g553155
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein; membrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-114/Domain: alpha-1 #status predicted <EX1>
F;115-206/Domain: alpha-2 #status predicted <EX2>
F;220-285/Domain: immunoglobulin homology <IMM>
F;307-331/Domain: transmembrane #status predicted <TMM>
F;110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;125-188,227-283/Disulfide bonds: #status predicted

Query Match 33.9%; Score 514; DB 2; Length 332;
Best Local Similarity 40.1%; Pred. No. 2.7e-35;
Matches 111; Conservative 43; Mismatches 115; Indels 8; Gaps 7;

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Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |     |   | |:|||||  || :| :  |:|:||| ||:      : |
Db         26 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
              | ::| |     ||  |:   :| |:: |||:|:: ||:: |     || :  |||
Db         85 DQETRSAKAHSQTDRVDLGTLRGYYNQSEDGSHTIQIMYGCDVGSDGRFLRGYRQDAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| :    |   | ||:  |  || :||     | | |||||  |   |:: || |:  |
Db        145 KDYIALNEDLRSWTAADMAAQITKRKWEAAH-AAEQQRAYLEGTCVEWLRRYLENGKETL 203

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :  ||   :||| ::    |||| || :||  ||: | :| :    :: |  :  | ||
Db        204 QRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGED-QTQDTELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |||||||| |:| || :|| : ||
Db        263 GTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE 299
```

RESULT 6
I36961
MHC class I protein - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C;Accession: I36961
R;Lawlor, D.A.; Warren, E.; Ward, F.E.; Parham, P.
Immunol. Rev. 113, 147-185, 1990
A;Title: Comparison of class I MHC alleles in humans and apes.
A;Reference number: I36961; MUID:90201944; PMID:1690682
A;Accession: I36961
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: GB:M30678; NID:g176822; PIDN:AAA87970.1; PID:g176823
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 33.8%; Score 511; DB 2; Length 365;
Best Local Similarity 39.7%; Pred. No. 5.3e-35;
Matches 110; Conservative 44; Mismatches 115; Indels 8; Gaps 7;

```
Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |     |   | |:|||||  || :| :  |:|:||| ||:      : |
Db         26 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
              : ::| |     ||  |:   :| |:: |||:|:: ||:: |     || :  |||
Db         85 DEETRSAKAHSQTDRVDLGTLRGYYNQSEDGSHTIQIMYGCDVGSDGRFLRGYRQDAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| :    |   | ||:  |  || :||     | | |||||  |   |:: || |:  |
Db        145 KDYIALNEDLRSWTAADMAAQITKRKWEAAH-AAEQRRAYLEGTCVEWLRRYLENGKETL 203

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :  ||   :||| ::    |||| || :||  ||: | :| :    :: |  :  | ||
Db        204 QRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGED-QTQDTELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |||||||| |:| || :|| : ||
Db        263 GTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE 299
```

RESULT 7
B27638
MHC class I histocompatibility antigen alpha chain precursor (BL3-7) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 16-Feb-1997
C;Accession: B27638
R;Ennis, P.D.; Jackson, A.P.; Parham, P.
J. Immunol. 141, 642-651, 1988
A;Title: Molecular cloning of bovine class I MHC cDNA.
A;Reference number: A92826; MUID:88258075; PMID:3133413
A;Accession: B27638
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-361 <ENN>
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: heterodimer; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-361/Product: MHC class I histocompatibility antigen, BoLA alpha chain (BL3-7) #sta
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 33.7%; Score 510; DB 2; Length 361;
Best Local Similarity 38.9%; Pred. No. 6.3e-35;
Matches 109; Conservative 49; Mismatches 114; Indels 8; Gaps 7;

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Qy          2 LLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISS 59
              |  |||| | : | |    ||    | |:|||||  || :| :  :  : | ||| ||:
Db         23 LAGSHSLRYFYTGVSRPGLGEPRFIAVGYVDDTQFVRFDSDAPNPREEPRVPWMEQE-GP 81

Qy         60 QMWLQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYG 117
              : | : ::  |    :| ||  |:   :| |:  || :| : ||::  |      |:|::|
Db         82 EYWDRNTRIYKDTAQIFRVDLNTLRGYYNQSETGSHNIQAMYGCDVGPDGRLLRGFWQFG 141

Qy        118 YDGQDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGR 177
              |||:| :    :   | ||:  |  || :||     |   | ||| :|   |:: || |:
Db        142 YDGRDYIALNEELRSWTAADTAAQITKRKWEAAG-AAETWRNYLEGECVEWLRRYLENGK 200

Qy        178 GVLDQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLP 236
              | :  ||   |||| ::    |||| || :||: |:: | :: :    :: |  :  |
Db        201 DTLLRADPPKAHVTHHSISDREVTLRCWALGFYPEEISLTWQREGED-QTQDMELVETRP 259

Qy        237 NGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              :||||:| |  | || ||||||||:|:| || :|| : ||
Db        260 SGDGTFQKWAALVVPSGEEQRYTCRVQHEGLQEPLTLRWE 299
```

RESULT 8

```
I83063
A11.2 - human
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: I83063
R;Lin, L.; Tokunaga, K.; Ishikawa, Y.; Bannai, M.; Kashiwase, K.; Kuwata, S.; Akaza, T.;
Tissue Antigens 43, 78-82, 1994
A;Title: Sequence analysis of serological HLA-A11 split antigens, A11.1 and A11.2.
A;Reference number: I60129; MUID:94287401; PMID:8016845
A;Accession: I83063
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: GB:D16842; NID:gS40517; PIDN:BAA04118.1; PID:g487911
C;Genetics:
A;Gene: A1102
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

  Query Match             33.6%;  Score 509;  DB 2;  Length 365;
  Best Local Similarity   39.4%;  Pred. No. 7.8e-35;
  Matches  109;  Conservative   46;  Mismatches  114;  Indels    8;  Gaps    7;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | :   |    |    | |:|||||  || :| :  |:|:||| ||:      : |
Db         26 SHSMRYFYTSVSRPGRGKPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
               | ::::|       ||  |:   :| |:: |||:|:: ||::  |      || :  |||
Db         85 DQETRNVKAQSQTDRVDLGTLRGYYNQSEDGSHTIQIMYGCDVGPDGRFLRGYRQDAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| :    |   | ||:  |  || :||     | | ||||| |   |:: || |: |
Db        145 KDYIALNEDLRSWTAADMAAQITKRKWEAAH-AAEQQRAYLEGRCVEWLRRYLENGKETL 203

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :  ||   :||| ::    |||| || :||  ||: | :| :    :: |  :  | ||
Db        204 QRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGED-QTQDTELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |||||||| |:| || :|| : ||
Db        263 GTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE 299


RESULT 9
A47636
MHC class I histocompatibility antigen HLA-A11 alpha chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 28-Apr-1995 #text_change 23-Jul-1999
C;Accession: S03536; S03694; A47636; I60129
R;Mayer, W.E.; Jonker, M.; Klein, D.; Ivanyi, P.; van Seventer, G.; Klein, J.
EMBO J. 7, 2765-2774, 1988
A;Title: Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-spec
A;Reference number: S01171; MUID:89030641; PMID:2460344
A;Accession: S03536
A;Molecule type: mRNA
A;Residues: 1-365 <MAY>
A;Cross-references: EMBL:X13111; NID:g32138; PIDN:CAA31503.1; PID:g32139
A;Note: this allele is designated A*1101 (formerly A11E, A11.1)
A;Accession: S03694
A;Molecule type: mRNA
A;Residues: 1-42,'K',44-298 <MA2>
A;Cross-references: EMBL:X13112; NID:g32142; PIDN:CAA31504.1; PID:g32143
A;Note: this allele is designated A*1102 (formerly A11K, A11.2)
R;Cowan, E.P.; Jelachich, M.L.; Biddison, W.E.; Coligan, J.E.
Immunogenetics 25, 241-250, 1987
A;Title: DNA sequence of HLA-A11: remarkable homology with HLA-A3 allows identification
A;Reference number: A47636; MUID:87192928; PMID:2437024
A;Accession: A47636
A;Molecule type: DNA
A;Residues: 26-365 <COW>
A;Cross-references: GB:M16007; GB:M16008; GB:M16009; GB:M16010; NID:g184130; PIDN:AAA654
A;Note: the authors translated the codon GAC for residue 89 as Ala, CCG for residue 104
A;Note: this allele is designated A*1101 (formerly A11E, A11.1)
R;Lin, L.; Tokunaga, K.; Ishikawa, Y.; Bannai, M.; Kashiwase, K.; Kuwata, S.; Akaza, T.
Tissue Antigens 43, 78-82, 1994
A;Title: Sequence analysis of serological HLA-A11 split antigens, A11.1 and A11.2.
A;Reference number: I60129; MUID:94287401; PMID:8016845
A;Accession: I60129
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: GB:D16841; NID:g540516; PIDN:BAA04117.1; PID:g487909
A;Note: this allele is designated A*1101 (formerly A11E, A11.1)
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-365/Product: class I histocompatibility antigen alpha chain #status predicted <MAT
F;25-298/Domain: extracellular #status predicted <EXT>
F;220-285/Domain: immunoglobulin homology <IMM>
F;299-337/Domain: transmembrane #status predicted <TMM>
F;338-365/Domain: intracellular #status predicted <INT>

  Query Match             33.6%;  Score 508;  DB 2;  Length 365;
  Best Local Similarity   39.4%;  Pred. No. 9.4e-35;
  Matches  109;  Conservative   46;  Mismatches  114;  Indels    8;  Gaps    7;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | :   |    |    | |:|||||  || :| :  |:|:||| ||:      : |
Db         26 SHSMRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
               | ::::|       ||  |:   :| |:: |||:|:: ||::  |      || :  |||
Db         85 DQETRNVKAQSQTDRVDLGTLRGYYNQSEDGSHTIQIMYGCDVGPDGRFLRGYRQDAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| :    |   | ||:  |  || :||     | | ||||| |   |:: || |: |
Db        145 KDYIALNEDLRSWTAADMAAQITKRKWEAAH-AAEQQRAYLEGRCVEWLRRYLENGKETL 203

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :  ||   :||| ::    |||| || :||  ||: | :| :    :: |  :  | ||
Db        204 QRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGED-QTQDTELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |||||||| |:| || :|| : ||
Db        263 GTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE 299


RESULT 10
I56039
HLA-A30.3 precursor - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I56039
R;Kato, K.; Trapani, J.A.; Allopenna, J.; Dupont, B.; Yang, S.Y.
J. Immunol. 143, 3371-3378, 1989
A;Title: Molecular analysis of the serologically defined HLA-Aw19 antigens. A genetical
A;Reference number: I56039; MUID:90038496; PMID:2478623
A;Accession: I56039
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-365 <RES>
A;Cross-references: GB:M30576; NID:g187646; PIDN:AAA59612.1; PID:g386878
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

  Query Match             33.6%;  Score 508;  DB 2;  Length 365;
  Best Local Similarity   39.4%;  Pred. No. 9.4e-35;
  Matches  109;  Conservative   47;  Mismatches  113;  Indels    8;  Gaps    7;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |    |   | |:|||||  || :| :  |:|:||| ||:      : |
```

```
Db         26 SHSMRYFFTSVSRPGSGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-RPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
              | ::::|       ||  |:   :| |:  |||:|:: ||::  |     || :: |||
Db         85 DQETRNVKAQSQTDRVDLGTLRGYYNQSEAGSHTIQIMYGCDVGSDGRFLRGYEQHAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| :    |   | ||:  |  |: :||  :  | | ||||  |   |:: || |:  |
Db        145 KDYIALNEDLRSWTAADMAAQITQRKWEAAR-WAEQLRAYLEGTCVEWLRRYLENGKETL 203

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :  ||   :||| ::    |||| || :||  ||: | :| :    :: |  :  | ||
Db        204 QRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGED-QTQDTELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |||||||| |:| || :|| : ||
Db        263 GTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE 299


RESULT 11
HLHUA3
MHC class I histocompatibility antigen HLA-A3 alpha chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 02-Sep-1997
C;Accession: A02192
R;Strachan, T.; Sodoyer, R.; Damotte, M.; Jordan, B.R.
EMBO J. 3, 887-894, 1984
A;Title: Complete nucleotide sequence of a functional class I HLA gene, HLA-A3: implicat
A;Reference number: A02192; MUID:84207948; PMID:6609814
A;Accession: A02192
A;Molecule type: DNA
A;Residues: 1-370 <STR>
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
A;Introns: 30/1; 120/1; 212/1; 304/1; 343/1; 354/1; 370/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantati
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-370/Product: class I histocompatibility antigen HLA-A3 alpha chain #status predicte
F;30-312/Domain: extracellular #status predicted <EXT>
F;30-119/Domain: alpha-1 <EX1>
F;120-211/Domain: alpha-2 <EX2>
F;225-290/Domain: immunoglobulin homology <IMM>
F;313-337/Domain: transmembrane #status predicted <TMM>
F;338-370/Domain: intracellular #status predicted <INT>
F;115/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;232-288/Disulfide bonds: #status predicted

  Query Match             33.4%;  Score 506;  DB 1;  Length 370;
  Best Local Similarity   39.6%;  Pred. No. 1.4e-34;
  Matches  110;  Conservative   46;  Mismatches  112;  Indels   10;  Gaps    8;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |    |   | |:|||||  || :| :  |:|:||| ||:      : |
Db         31 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 89

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
              | ::::|       ||  |:   :| |:  |||:|:: ||::  |     || :  |||
Db         90 DQETRNVKAQSQTDRVDLGTLRGYYNQSEAGSHTIQIMYGCDVGSDGRFLRGYRQDAYDG 149

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWE-RHKIRARQNRAYLERDCPAQLQQLLELGRGV 179
              :| :    |   | ||:  |  || :||  |:  | | ||||:  |   |:: || |:
Db        150 KDYIALNEDLRSWTAADMAAQITKRKWEAAHE--AEQLRAYLDGTCVEWLRRYLENGKET 207

Qy        180 LDQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNG 238
              | :  ||   :||| ::    |||| || :||  ||: | :| :    :: |  :  | |
Db        208 LQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGED-QTQDTELVETRPAG 266

Qy        239 DGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||:| |  : || |||||||| |:| || :|| : ||
Db        267 DGTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE 304


RESULT 12
I38439
MHC class I histocompatibility antigen HLA-A*8001 precursor - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 21-Jan-2000
C;Accession: I59638; I38439
R;Domena, J.D.; Hildebrand, W.H.; Bias, W.B.; Parham, P.
Tissue Antigens 42, 156-159, 1993
A;Title: A sixth family of HLA-A alleles defined by HLA-A*8001.
A;Reference number: I59638; MUID:94112691; PMID:8284791
A;Accession: I59638
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-365 <DOM>
A;Cross-references: GB:L18898; NID:g306853; PIDN:AAA17012.1; PID:g306854
R;Balas, A.; Garcia-Sanchez, F.; Gomez-Reino, F.; Vicario, J.L.
Immunogenetics 39, 452, 1994
A;Title: Characterization of a new and highly distinguishable HLA-A allele in a Spanish
A;Reference number: I38439; MUID:94245293; PMID:8188325
A;Accession: I38439
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-365 <BAL>
A;Cross-references: EMBL:U03754; NID:g432407; PIDN:AAC04322.1; PID:g432408
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

  Query Match             33.3%;  Score 504;  DB 2;  Length 365;
  Best Local Similarity   38.3%;  Pred. No. 2e-34;
  Matches  106;  Conservative   52;  Mismatches  111;  Indels    8;  Gaps    7;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |    |   | |:|||||  || :| :  |:|:||| ||:      : |
Db         26 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDSQFVQFDSDAASQRMEPRAPWIEQE-EPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
              : ::::|       :  |:   :| |:: |||:|:: ||::  |     || :  |||
Db         85 DEETRNVKAHSQTNRANLGTLRGYYNQSEDGSHTIQIMYGCDVGSDGRFLRGYRQDAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| :    |   | ||:  |  || :||  : || | ||||| :|   |:: || |:  |
Db        145 KDYIALNEDLRSWTAADMAAQITKRKWEAAR-RAEQLRAYLEGECVDGLRRYLENGKETL 203

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :  ||   :||| ::    |||| ||::||  ||: | :| :    :: |  :  | ||
Db        204 QRTDPPKTHMTHHPISDHEATLRCWALSFYPAEITLTWQRDGED-QTQDTELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |:|:|||| |:| || :|| : ||
Db        263 GTFQKWAAVVVPSGKEKRYTCHVQHEGLPEPLTLRWE 299


RESULT 13
I37542
MHC class I histocompatibility antigen HLA-A2 alpha chain (allele A*0216) precursor - h
C;Species: Homo sapiens (man)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C;Accession: I37542; S49582
R;Barouch, D.; Krausa, P.; Bodmer, J.; Browning, M.J.; McMichael, A.J.
Immunogenetics 41, 388, 1995
A;Title: Identification of a novel HLA-A2 subtype, HLA-A*0216.
A;Reference number: I37542; MUID:95278976; PMID:7759139
A;Accession: I37542
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: EMBL:Z46633; NID:g575248; PIDN:CAA86602.1; PID:g575249
```

A;Note: submitted to the EMBL Data Library, November 1994
C;Genetics:
A;Gene: hla-A
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 33.2%; Score 503; DB 2; Length 365;
Best Local Similarity 39.4%; Pred. No. 2.5e-34;
Matches 109; Conservative 45; Mismatches 115; Indels 8; Gaps 7;

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Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |     |   | |:|||||  || :| :  |:|:||| ||:      : |
Db         26 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQED-NSTEGYWKYGYDG 120
                :: :|       ||  |:   :| |:  |||:| : ||::  |      || :| |||
Db         85 DGETRKVKAHSQTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDVGSDWRFLRGYHQYAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| :   |  | ||:  |  || :||   : | | ||||| :|   |:: || |:  |
Db        145 KDYIALKEDLRSWTAADMAAQTTKHKWEAAHV-AEQLRAYLEGECVEWLRRYLENGKETL 203

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
               :   |   :||| |:    |||| ||::||  ||: | :| :    :: |  :  | ||
Db        204 QRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGED-QTQDTELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |:|||||| |:| || :|| : ||
Db        263 GTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRWE 299
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RESULT 14
I38442
gene HLA-A-0205 protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I38442
R;Holmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P.
J. Immunol. 139, 936-941, 1987
A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A2
A;Reference number: I38441; MUID:87252273; PMID:3496393
A;Accession: I38442
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-365 <RES>
A;Cross-references: EMBL:U03862; NID:g432436; PIDN:AAA03603.1; PID:g432437
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 33.2%; Score 503; DB 2; Length 365;
Best Local Similarity 39.7%; Pred. No. 2.5e-34;
Matches 110; Conservative 43; Mismatches 116; Indels 8; Gaps 7;

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Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | :   |     |   | |:|||||  || :| :  |||:||| ||:      : |
Db         26 SHSMRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASRRMEPRAPWIEQE-GPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQED-NSTEGYWKYGYDG 120
                :: :|       ||  |:   :| |:  |||||  : ||::  |      || :| |||
Db         85 DGETRKVKAHSQTHRVDLGTLRGYYNQSEAGSHTLQRMYGCDVGSDWRFLRGYHQYAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| :   |  | ||:  \  || :||   : | | |||||  |   |:: || |:  |
Db        145 KDYIALKEDLRSWTAADMAAQTTKHKWEAAHV-AEQWRAYLEGTCVEWLRRYLENGKETL 203

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
               :   |   :||| |:    |||| ||::||  ||: | :| :    :: |  :  | ||
Db        204 QRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGED-QTQDTELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |:|||||| |:| || :|| : ||
Db        263 GTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRWE 299
```

RESULT 15
I61902
MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate A*0
C;Species: Homo sapiens (man)
A;Variety: isolate A*0212
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999
C;Accession: I61902
R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.;
Nature 357, 326-329, 1992
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A;Reference number: I37120; MUID:92269955; PMID:1317015
A;Accession: I61902
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: GB:M84378; NID:g187625; PIDN:AAA59604.1; PID:g187626
A;Experimental source: cell line KRC 033; isolate A*0212
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status pred
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 33.2%; Score 503; DB 2; Length 365;
Best Local Similarity 39.4%; Pred. No. 2.5e-34;
Matches 109; Conservative 44; Mismatches 116; Indels 8; Gaps 7;

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Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |     |   | |:|||||  || :| :  |:|:||| ||:      : |
Db         26 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQED-NSTEGYWKYGYDG 120
                :: :|       ||  |:   :| |:  |||:| : ||::  |      || :| |||
Db         85 DGETRKVKAHSQTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDVGSDWRFLRGYHQYAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| :   |  | ||:  |  || :||   : | | |||||  |   |:: || |:  |
Db        145 KDYIALKEDLRSWTAADMAAQTTKHKWEAAHV-AEQQRAYLEGTCVEWLRRYLENGKETL 203

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
               :   |   :||| |:    |||| ||::||  ||: | :| :    :: |  :  | ||
Db        204 QRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGED-QTQDTELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |:|||||| |:| || :|| : ||
Db        263 GTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRWE 299
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Search completed: May 4, 2004, 11:39:26
Job time : 14.6667 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 4, 2004, 11:32:18 ; Search time 8.33333 Seconds
(without alignments)
1724.564 Million cell updates/sec

Title: US-10-092-404-3
Perfect score: 1514
Sequence: 1 RLLRSHSLHYLFMGASEQDL.....RYTCQVEHPGLDQPLIVIWE 276

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1502	99.2	348	1	HFE_HUMAN	Q30201 homo sapien
2	1502	99.2	348	1	HFE_PANTR	P60018 pan troglod
3	1227	81.0	348	1	HFE_DICSU	Q9gl42 dicerorhinu
4	1225	80.9	348	1	HFE_CERSI	Q9gkz0 ceratotheri
5	1221	80.6	348	1	HFE_RHIUN	Q9gl41 rhinoceros
6	1218	80.4	348	1	HFE_DICBI	Q9gl43 diceros bic
7	1145	75.6	360	1	HFE_RAT	O35799 rattus norv
8	1129	74.6	359	1	HFE_MOUSE	P70387 mus musculu
9	517	34.1	361	1	HA1A_RABIT	P01894 oryctolagus
10	517	34.1	361	1	HA1B_RABIT	P06140 oryctolagus
11	511	33.8	365	1	1A01_PANTR	P16209 pan troglod
12	510	33.7	364	1	HA1B_BOVIN	P13753 bos taurus
13	508	33.6	365	1	1A11_HUMAN	P13746 homo sapien
14	506	33.4	365	1	1A03_HUMAN	P04439 homo sapien
15	504	33.3	365	1	1A80_HUMAN	Q09160 homo sapien
16	502	33.2	365	1	1A31_HUMAN	P16189 homo sapien
17	500	33.0	365	1	1A02_HUMAN	P01892 homo sapien
18	500	33.0	365	1	1A30_HUMAN	P16188 homo sapien
19	500	33.0	365	1	1A74_HUMAN	P30459 homo sapien
20	498	32.9	365	1	1A03_PANTR	P13748 pan troglod
21	497	32.8	365	1	1A33_HUMAN	P16190 homo sapien
22	497	32.8	365	1	1A36_HUMAN	P30455 homo sapien
23	497	32.8	365	1	1A68_HUMAN	P01891 homo sapien
24	495.5	32.7	362	1	HA19_CANFA	P18466 canis famil
25	495	32.7	365	1	1A01_HUMAN	P30443 homo sapien
26	494	32.6	273	1	1A69_HUMAN	P10316 homo sapien
27	494	32.6	296	1	ZA2G_RAT	Q63678 rattus norv
28	494	32.6	365	1	1A04_PANTR	P13749 pan troglod
29	494	32.6	365	1	1A24_HUMAN	P05534 homo sapien
30	492	32.5	360	1	HA1A_BOVIN	P13752 bos taurus
31	491	32.4	362	1	1B47_HUMAN	P30485 homo sapien
32	490	32.4	365	1	1A23_HUMAN	P30447 homo sapien
33	487	32.2	363	1	1B04_GORGO	P30382 gorilla gor
34	486	32.1	295	1	ZA2G_HUMAN	P25311 homo sapien
35	486	32.1	322	1	HA10_MOUSE	P01898 mus musculu
36	486	32.1	362	1	1B37_HUMAN	P18463 homo sapien
37	486	32.1	371	1	HA12_RAT	P16391 rattus norv
38	485	32.0	365	1	1A34_HUMAN	P30453 homo sapien
39	485	32.0	365	1	1A66_HUMAN	P30457 homo sapien
40	484	32.0	338	1	HLAG_HUMAN	P17693 homo sapien
41	484	32.0	362	1	1B27_HUMAN	P03989 homo sapien
42	484	32.0	366	1	1C02_GORGO	P30385 gorilla gor
43	484	32.0	366	1	1C04_GORGO	P30387 gorilla gor
44	483	31.9	359	1	1B01_PANTR	P13750 pan troglod
45	483	31.9	365	1	1A01_PONPY	P16211 pongo pygma

ALIGNMENTS

RESULT 1
HFE_HUMAN
ID HFE_HUMAN STANDARD; PRT; 348 AA.
AC Q30201; O75929; O75930; O75931; Q96KU5; Q96KU7; Q96KU8; Q9HC64;
AC Q9HC68; Q9HC70; Q9HC83;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hereditary hemochromatosis protein precursor (HLA-H).
GN HFE OR HLAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS HH ASP-63 AND TYR-282.
RX MEDLINE=96331279; PubMed=8696333;
RA Feder J.N., Gnirke A., Thomas W., Tsuchihashi Z., Ruddy D.A.,
RA Basava A., Dormishian F., Domingo R., Ellis M.C. Jr., Fullan A.,
RA Hinton L.M., Jones N.L., Kimmel B.E., Kronmal G.S., Lauer P.,
RA Lee V.K., Loeb D.B., Mapa F.A., McClelland E., Meyer N.C.,
RA Mintier G.A., Moeller N., Moore T., Morikang E., Prass C.E.,
RA Quintana L., Starnes S.M., Schatzman R.C., Brunke K.J.,
RA Drayna D.T., Risch N.J., Bacon B.R., Wolff R.K.;
RT "A novel MHC class I-like gene is mutated in patients with hereditary
RT haemochromatosis.";
RL Nat. Genet. 13:399-409(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Albig W., Burmester N., Bode C., Doenecke D., Drabent B.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=97294057; PubMed=9149941;
RA Ruddy D.A., Kronmal G.S., Lee V.K., Mintier G.A., Quintana L.,
RA Domingo R. Jr., Meyer N.C., Irrinki A., McClelland E.E., Fullan A.,
RA Mapa F.A., Moore T., Thomas W., Loeb D.B., Harmon C., Tsuchihashi Z.,
RA Wolff R.K., Schatzman R.C., Feder J.N.;
RT "A 1.1-Mb transcript map of the hereditary hemochromatosis locus.";
RL Genome Res. 7:441-456(1997).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Gasparini P.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4).
RX MEDLINE=99180629; PubMed=10079302;
RA Rhodes D.A., Trowsdale J.;
RT "Alternate splice variants of the hemochromatosis gene Hfe.";
RL Immunogenetics 49:357-359(1999).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORMS 2; 5; 6 AND 7).
RA Oliva R., Sanchez M.;
RT "Identification of different alternative splicing forms of the HFE
RT gene.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

```
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 7; 8; 9 AND 10).
RX   MEDLINE=20448010; PubMed=11001625;
RA   Thenie A., Orhant M., Gicquel I., Fergelot P., Le Gall J.-Y.,
RA   David V., Mosser J.;
RT   "The HFE gene undergoes alternate splicing processes.";
RL   Blood Cells Mol. Dis. 26:155-162(2000).
RN   [8]
RP   FUNCTION.
RX   MEDLINE=98132614; PubMed=9465039;
RA   Feder J.N., Penny D.M., Irrinki A., Lee V.K., Lebron J.A., Watson N.,
RA   Tsuchihashi Z., Sigal E., Bjorkman P.J., Schatzman R.C.;
RT   "The hemochromatosis gene product complexes with the transferrin
RT   receptor and lowers its affinity for ligand binding.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:1472-1477(1998).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX   MEDLINE=98206473; PubMed=9546397;
RA   Lebron J.A., Bennett M.J., Vaughn D.E., Chirino A.J., Snow P.M.,
RA   Mintier G.A., Feder J.N., Bjorkman P.J.;
RT   "Crystal structure of the hemochromatosis protein HFE and
RT   characterization of its interaction with transferrin receptor.";
RL   Cell 93:111-123(1998).
RN   [10]
RP   VARIANTS HH ASP-63 AND TYR-282.
RX   MEDLINE=97260408; PubMed=9106528;
RA   Carella M., D'Ambrosio L., Totaro A., Grifa A., Valentino M.A.,
RA   Piperno A., Girelli D., Roetto A., Franco B., Gasparini P.,
RA   Camaschella C.;
RT   "Mutation analysis of the HLA-H gene in Italian hemochromatosis
RT   patients.";
RL   Am. J. Hum. Genet. 60:828-832(1997).
RN   [11]
RP   VARIANT HH/PCT TYR-282.
RX   MEDLINE=97176837; PubMed=9024376;
RA   Roberts A.G., Whatley S.D., Morgan R.R., Worwood M., Elder G.H.;
RT   "Increased frequency of the haemochromatosis Cys282Tyr mutation in
RT   sporadic porphyria cutanea tarda.";
RL   Lancet 349:321-323(1997).
RN   [12]
RP   VARIANT HH/PCT ASP-63.
RX   MEDLINE=98085904; PubMed=9425935;
RA   Sampietro M., Piperno A., Lupica L., Arosio C., Vergani A.,
RA   Corbetta N., Malosio I., Mattioli M., Fracanzani A.L.,
RA   Cappellini M.D., Fiorelli G., Fargion S.;
RT   "High prevalence of the His63Asp HFE mutation in Italian patients with
RT   porphyria cutanea tarda.";
RL   Hepatology 27:181-184(1998).
RN   [13]
RP   VARIANTS HH/PCT ASP-63 AND TYR-282.
RX   MEDLINE=98281650; PubMed=9620340;
RA   Bonkovsky H.L., Poh-Fitzpatrick M., Pimstone N., Obando J.,
RA   Di Bisceglie A., Tattrie C., Tortorelli K., LeClair P., Mercurio M.G.,
RA   Lambrecht R.W.;
RT   "Porphyria cutanea tarda, hepatitis C, and HFE gene mutations in North
RT   America.";
RL   Hepatology 27:1661-1669(1998).
RN   [14]
RP   VARIANTS HH ASP-63; CYS-65 AND TYR-282.
RX   MEDLINE=99211934; PubMed=10194428;
RA   Mura C., Raguenes O., Ferec C.;
RT   "HFE mutations analysis in 711 hemochromatosis probands: evidence for
RT   S65C implication in mild form of hemochromatosis.";
RL   Blood 93:2502-2505(1999).
RN   [15]
RP   VARIANTS HH CYS-65; ARG-93 AND THR-105.
RX   MEDLINE=20042794; PubMed=10575540;
RA   Barton J.C., Sawada-Hirai R., Rothenberg B.E., Acton R.T.;
RT   "Two novel missense mutations of the HFE gene (I105T and G93R) and
RT   identification of the S65C mutation in Alabama hemochromatosis
RT   probands.";
RL   Blood Cells Mol. Dis. 25:147-155(1999).
RN   [16]
RP   VARIANTS VP ASP-63 AND HIS-127, VARIANT HH MET-330, AND VARIANTS
RP   MET-53 AND MET-59.
RX   MEDLINE=99330560; PubMed=10401000;
RA   de Villiers J.N.P., Hillermann R., Loubser L., Kotze M.J.;
RT   "Spectrum of mutations in the HFE gene implicated in haemochromatosis
RT   and porphyria.";
RL   Hum. Mol. Genet. 8:1517-1522(1999).
RN   [17]
RP   VARIANTS HH ASP-63 AND TYR-282.
RX   MEDLINE=99140260; PubMed=10094552;
RA   Merryweather-Clarke A.T., Simonsen H., Shearman J.D., Pointon J.J.,
RA   Norgaard-Pedersen B., Robson K.J.H.;
RT   "A retrospective anonymous pilot study in screening newborns for HFE
RT   mutations in Scandinavian populations.";
RL   Hum. Mutat. 13:154-159(1999).
RN   [18]
RP   VARIANT HH CYS-65.
RA   Fagan E., Payne S.J.;
RT   "A novel missense mutation S65C in the HFE gene with a possible role
RT   in hereditary haemochromatosis.";
RL   Hum. Mutat. 13:507-508(1999).
RN   [19]
RP   VARIANT LYS-277.
RX   MEDLINE=20081073; PubMed=10612845;
RA   Bradbury R., Fagan E., Payne S.J.;
RT   "Two novel polymorphisms (E277K and V212V) in the haemochromatosis
RT   gene HFE.";
RL   Hum. Mutat. 15:120-120(2000).
CC   -!- FUNCTION: Binds to transferrin receptor (TFR) and reduces its
CC       affinity for iron-loaded transferrin.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=10;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1;
CC         IsoId=Q30201-1; Sequence=Displayed;
CC       Name=2; Synonyms=delE2;
CC         IsoId=Q30201-2; Sequence=VSP_003218;
CC       Name=3; Synonyms=del14E4;
CC         IsoId=Q30201-3; Sequence=VSP_003225;
CC       Name=4; Synonyms=delE214E4;
CC         IsoId=Q30201-4; Sequence=VSP_003218, VSP_003225;
CC       Name=5;
CC         IsoId=Q30201-5; Sequence=VSP_003219;
CC       Name=6;
CC         IsoId=Q30201-6; Sequence=VSP_003220;
CC       Name=7; Synonyms=delE3;
CC         IsoId=Q30201-7; Sequence=VSP_003221;
CC       Name=8; Synonyms=1043-2283del,intron6ins;
CC         IsoId=Q30201-8; Sequence=VSP_003226, VSP_003227;
CC       Name=9; Synonyms=delE3-7;
CC         IsoId=Q30201-9; Sequence=VSP_003223, VSP_003224;
CC       Name=10; Synonyms=562-878del;
CC         IsoId=Q30201-10; Sequence=VSP_003222;
CC   -!- TISSUE SPECIFICITY: In all tissues tested except brain.
CC   -!- DISEASE: Defects in HFE are a cause of hereditary hemochromatosis
CC       (HH) [MIM:235200]. HH is an autosomal recessive inborn disorder of
CC       iron metabolism, frequent among caucasians. HH is characterized by
CC       abnormal intestinal iron absorption and progressive increase of
CC       total body iron, which results in midlife in clinical
CC       complications including cirrhosis, cardiopathy, diabetes,
CC       endocrine dysfunctions, arthropathy, and susceptibility to liver
CC       cancer. Since the disease complications can be effectively
CC       prevented by regular phlebotomies, early diagnosis is most
CC       important to provide a normal life expectancy to the affected
CC       subjects.
CC   -!- DISEASE: Defects in HFE are a cause of porphyria cutanea tarda
CC       (PCT), a disorder characterized by light-sensitive dermatitis and
CC       presence of large amounts of uroporphyrin in urine. Iron overload
CC       is often present in association with varying degrees of liver
CC       damage. PCT is the most common form of porphyria worldwide. It
CC       occurs in two forms: the sporadic type (PCT type I) and the
CC       familial type (PCT type II), which is inherited in an autosomal
```

```
  Query Match             99.2%;  Score 1502;  DB 1;  Length 348;
  Best Local Similarity   99.3%;  Pred. No. 1.5e-116;
  Matches  274;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298
```

```
RESULT 2
HFE_PANTR
ID   HFE_PANTR      STANDARD;      PRT;   348 AA.
AC   P60018;
DT   15-MAR-2004 (Rel. 43, Created)
DT   15-MAR-2004 (Rel. 43, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Hereditary hemochromatosis protein precursor (HLA-H).
GN   HFE OR HLAH.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22184165; PubMed=12196404;
RA   Toomajian C., Kreitman M.;
RT   "Sequence variation and haplotype structure at the Human HFE Locus.";
RL   Genetics 161:1609-1623(2002).
CC   -!- FUNCTION: Binds to transferrin receptor (TFR) and reduces its
CC       affinity for iron-loaded transferrin (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: TO MHC CLASS I ANTIGENS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF447807; AAN09793.1; -.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   MHC I; Transmembrane; Glycoprotein; Transport; Iron transport; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    348       HEREDITARY HEMOCHROMATOSIS PROTEIN.
FT   DOMAIN       23    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      115    205       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      206    297       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      298    306       CONNECTING PEPTIDE.
FT   TRANSMEM    307    330       POTENTIAL.
FT   DOMAIN      331    348       CYTOPLASMIC TAIL.
FT   DISULFID    124    187       BY SIMILARITY.
FT   DISULFID    225    282       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    130    130       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    234    234       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   348 AA;  40108 MW;  432EB9A314A55BEA CRC64;
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  Query Match             99.2%;  Score 1502;  DB 1;  Length 348;
  Best Local Similarity   99.3%;  Pred. No. 1.5e-116;
  Matches  274;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298
```

```
RESULT 3
HFE_DICSU
ID   HFE_DICSU      STANDARD;      PRT;   348 AA.
AC   Q9GL42;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hereditary hemochromatosis protein precursor.
GN   HFE.
OS   Dicerorhinus sumatrensis (Sumatran rhinoceros).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Dicerorhinus.
OX   NCBI_TaxID=89632;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   West C.J., Worley M., Beutler E.;
RT   "Rhinoceros HFE polymorphisms.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Binds to transferrin receptor (TFR) and reduces its
CC       affinity for iron-loaded transferrin.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: TO MHC CLASS I ANTIGENS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY007543; AAG23703.1; -.
DR   HSSP; Q30201; 1A6Z.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
```

```
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    348       HEREDITARY HEMOCHROMATOSIS PROTEIN.
FT   DOMAIN       23    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      115    205       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      206    297       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      298    306       CONNECTING PEPTIDE.
FT   TRANSMEM    307    330       POTENTIAL.
FT   DOMAIN      331    348       CYTOPLASMIC TAIL.
FT   DISULFID    124    187       BY SIMILARITY.
FT   DISULFID    225    282       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    130    130       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    234    234       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   348 AA;  39740 MW;  518BFD357AB83B90 CRC64;

  Query Match             81.0%;  Score 1227;  DB 1;  Length 348;
  Best Local Similarity   81.0%;  Pred. No. 6.5e-94;
  Matches  221;  Conservative   20;  Mismatches   32;  Indels    0;  Gaps    0;

Qy          4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWL 63
              ||||| |||||||:| || |||||||||:||| |:||||| | |  ||     ||:||
Db         26 RSHSLRYLFMGASERDHGLPLFEALGYVDDELFVAYNHESRRAESRAQWVLGEAHSQLWL 85

Qy         64 QLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDA 123
              |||||||||||| |||||||:||| ||||||||||||||:|||||| |:|||||||||
Db         86 QLSQSLKGWDHMFIVDFWTIMDNHNHSKESHTLQVILGCEVQEDNSTRGFWKYGYDGQDH 145

Qy        124 LEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQ 183
              |||||:|||||||| ||  |||||| :||||:|||||||||| ||| ||||||||||||
Db        146 LEFCPETLDWRAAESRALTTKLEWEVNKIRAKQNRAYLERDCPEQLQWLLELGRGVLDQQ 205

Qy        184 VPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQ 243
              |||||||||||  |:||||||:|||:|||||||:||||::|:|  |: | |||||:||||||
Db        206 VPPLVKVTHHVASAVTTLRCQALNFYPQNITMRWLKDRKPVDVKDAESKDVLPSGDGTYQ 265

Qy        244 GWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |: |||||||||||||||||||||||||   ||
Db        266 SWVALAVPPGEEQRYTCQVEHPGLDQPLTATWE 298


RESULT 4
HFE_CERSI
ID   HFE_CERSI      STANDARD;      PRT;   348 AA.
AC   Q9GKZ0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hereditary hemochromatosis protein precursor.
GN   HFE.
OS   Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX   NCBI_TaxID=9807;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   West C.J., Worley M., Beutler E.;
RT   "Rhinoceros HFE polymorphisms.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Binds to transferrin receptor (TFR) and reduces its
CC       affinity for iron-loaded transferrin.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: TO MHC CLASS I ANTIGENS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY007541; AAG23701.1; -.
DR   HSSP; Q30201; 1A6Z.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    348       HEREDITARY HEMOCHROMATOSIS PROTEIN.
FT   DOMAIN       23    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      115    205       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      206    297       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      298    306       CONNECTING PEPTIDE.
FT   TRANSMEM    307    330       POTENTIAL.
FT   DOMAIN      331    348       CYTOPLASMIC TAIL.
FT   DISULFID    124    187       BY SIMILARITY.
FT   DISULFID    225    282       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    130    130       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    234    234       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   348 AA;  39822 MW;  2523016ECE9FBE91 CRC64;

  Query Match             80.9%;  Score 1225;  DB 1;  Length 348;
  Best Local Similarity   81.3%;  Pred. No. 9.5e-94;
  Matches  222;  Conservative   18;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWL 63
              ||||| |||||||:| || |||||||||:||| |:||||| | |  ||     ||:||
Db         26 RSHSLRYLFMGASERDHGLPLFEALGYVDDELFVAYNHESRRAESRAQWVLGEAHSQLWL 85

Qy         64 QLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDA 123
              |||||||||||| |||||||:||| ||||||||||||||:|||||| |:|||||||||
Db         86 QLSQSLKGWDHMFIVDFWTIMDNHNHSKESHTLQVILGCEVQEDNSTRGFWKYGYDGQDH 145

Qy        124 LEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQ 183
              |||||:|||||||| ||  |||||| :||||:|||||||||| ||| ||||||||||||
Db        146 LEFCPETLDWRAAESRALTTKLEWEVNKIRAKQNRAYLERDCPEQLQWLLELGRGVLDQQ 205

Qy        184 VPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQ 243
              |||||||||||  |:||||||:|||:|||||||:||||::|:|  |: | |||||:||||||
Db        206 VPPLVKVTHHVASAVTTLRCQALNFYPQNITMRWLKDRKPMDVKDAESKDVLPSGDGTYQ 265

Qy        244 GWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |: |||||||||||||||||||||||||   ||
Db        266 SWEALAVPPGEEQRYTCQVEHPGLDQPLTATWE 298


RESULT 5
HFE_RHIUN
ID   HFE_RHIUN      STANDARD;      PRT;   348 AA.
AC   Q9GL41;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hereditary hemochromatosis protein precursor.
GN   HFE.
OS   Rhinoceros unicornis (Greater Indian rhinoceros).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Rhinoceros.
OX   NCBI_TaxID=9809;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   West C.J., Worley M., Beutler E.;
RT   "Rhinoceros HFE polymorphisms.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Binds to transferrin receptor (TFR) and reduces its
CC       affinity for iron-loaded transferrin.
```

```
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: TO MHC CLASS I ANTIGENS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY007544; AAG23704.1; -.
DR   HSSP; Q30201; 1A6Z.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    348       HEREDITARY HEMOCHROMATOSIS PROTEIN.
FT   DOMAIN       23    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      115    205       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      206    297       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      298    306       CONNECTING PEPTIDE.
FT   TRANSMEM    307    330       POTENTIAL.
FT   DOMAIN      331    348       CYTOPLASMIC TAIL.
FT   DISULFID    124    187       BY SIMILARITY.
FT   DISULFID    225    282       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    130    130       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    234    234       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   348 AA;  39743 MW;  F2723D57A327A6B4 CRC64;

  Query Match             80.6%;  Score 1221;  DB 1;  Length 348;
  Best Local Similarity   80.6%;  Pred. No. 2e-93;
  Matches  220;  Conservative   20;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWL 63
              ||||| |||||||:| || |||||||||:||| |:||||| | |  ||     ||:||
Db         26 RSHSLRYLFMGASERDHGLPLFEALGYVDDELFVAYNHESRRAESRAQWVLGEAHSQLWL 85

Qy         64 QLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDA 123
              ||||||||||||| |||||||:||| |||||||||||||:|||||| |:| |||||||
Db         86 QLSQSLKGWDHMFIVDFWTIMDNHNHSKESHTLQVILGCEVQEDNSTRGFWMYGYDGQDH 145

Qy        124 LEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQ 183
              |||||:|||||||| ||  |||||| :||||:|||||||||||| ||| ||||||||||||
Db        146 LEFCPETLDWRAAESRALTTKLEWEVNKIRAKQNRAYLERDCPEQLQWLLELGRGVLDQQ 205

Qy        184 VPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQ 243
              |||||||||||  |:|||||:|||:|||||||:||||::|:|  |: | |||||:||||||
Db        206 VPPLVKVTHHVASAVTTLRCQALNFYPQNITMRWLKDRKPVDVKDAESKDVLPSGDGTYQ 265

Qy        244 GWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |: |||||||||||||||||||||||||||   ||
Db        266 SWVALAVPPGEEQRYTCQVEHPGLDQPLTATWE 298


RESULT 6
HFE_DICBI
ID   HFE_DICBI      STANDARD;      PRT;   348 AA.
AC   Q9GL43; Q9GK81;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hereditary hemochromatosis protein precursor.
GN   HFE.
OS   Diceros bicornis (Black rhinoceros).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Diceros.
OX   NCBI_TaxID=9805;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   West C.J., Worley M., Beutler E.;
RT   "Rhinoceros HFE polymorphisms.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Binds to transferrin receptor (TFR) and reduces its
CC       affinity for iron-loaded transferrin.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: TO MHC CLASS I ANTIGENS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY007542; AAG23702.1; -.
DR   EMBL; AF301592; AAG39940.1; -.
DR   HSSP; Q30201; 1A6Z.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    348       HEREDITARY HEMOCHROMATOSIS PROTEIN.
FT   DOMAIN       23    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      115    205       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      206    297       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      298    306       CONNECTING PEPTIDE.
FT   TRANSMEM    307    330       POTENTIAL.
FT   DOMAIN      331    348       CYTOPLASMIC TAIL.
FT   DISULFID    124    187       BY SIMILARITY.
FT   DISULFID    225    282       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    130    130       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    234    234       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   348 AA;  39818 MW;  4D95E7B01E48FB90 CRC64;

  Query Match             80.4%;  Score 1218;  DB 1;  Length 348;
  Best Local Similarity   80.6%;  Pred. No. 3.6e-93;
  Matches  220;  Conservative   20;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWL 63
              ||||| |||||||:| || |||||||||:||| |:||||| | |  ||     ||:||
Db         26 RSHSLRYLFMGASERDHGLPLFEALGYVDDELFVAYNHESRRAESRAQWVLGEAHSQLWL 85

Qy         64 QLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDA 123
              ||:|||||||| |||||||:||| |||||||||||||:|||||| |:|||||||
Db         86 QLTQSLKGWDHMFIVDFWTIMDNHNHSKESHTLQVILGCEVQEDNSTRGFWKYGYDGQDH 145

Qy        124 LEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQ 183
              |||||:|||||||| ||  |||||| :||||:|||||||||||| ||| ||||||||||||
Db        146 LEFCPETLDWRAAESRALTTKLEWEVNKIRAKQNRAYLERDCPEQLQWLLELGRGVLDQQ 205

Qy        184 VPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQ 243
              |||||||||||  |:|||||:|||:|||||||:||||::|:|  |: | |||||:||||||
Db        206 VPPLVKVTHHVASAVTTLRCQALNFYPQNITMRWLKDRKPVDVKDAESKDVLPSGDGTYQ 265
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Qy        244 GWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
                |  ||||||||||||||||||||||||||   ||
Db        266 SWEALAVPPGEEQRYTCQVEHPGLDQPLTATWE 298


RESULT 7
HFE_RAT
ID   HFE_RAT        STANDARD;      PRT;   360 AA.
AC   O35799; O35175;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hereditary hemochromatosis protein homolog precursor (RT1-CAFE).
GN   HFE.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Banasch M.W., Schaefer H., Schmidt W.E.;
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 42-303 FROM N.A.
RC   TISSUE=Small intestine;
RA   Sawada-Hirai R., Rothenberg B.E.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Binds to transferrin receptor (TFR) and reduces its
CC       affinity for iron-loaded transferrin (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: TO MHC CLASS I ANTIGENS.
CC   ---------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AJ001517; CAA04799.1; -.
DR   EMBL; AF008587; AAB86597.1; -.
DR   HSSP; Q30201; 1A6Z.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     25       POTENTIAL.
FT   CHAIN        26    360       HEREDITARY HEMOCHROMATOSIS PROTEIN
FT                                HOMOLOG.
FT   DOMAIN       26    127       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      128    218       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      219    310       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      311    319       CONNECTING PEPTIDE.
FT   TRANSMEM    320    340       POTENTIAL.
FT   DOMAIN      341    360       CYTOPLASMIC TAIL.
FT   DISULFID    137    200       BY SIMILARITY.
FT   DISULFID    238    295       BY SIMILARITY.
FT   CARBOHYD    115    115       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    143    143       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    167    167       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    247    247       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    198    198       R -> K (IN REF. 2).
SQ   SEQUENCE   360 AA;  40988 MW;  CC819834EE3240B3 CRC64;

  Query Match             75.6%;  Score 1145;  DB 1;  Length 360;
  Best Local Similarity   73.2%;  Pred. No. 3.9e-87;
  Matches  205;  Conservative   29;  Mismatches   38;  Indels    8;  Gaps    1;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQ 64
              |||| |||||||: ||||  |||||||||||||| |:|||||| ||| ||:  : |||:|||
Db         32 SHSLRYLFMGASKPDLGLPFFEALGYVDDQLFVSYNHESRRAEPRAPWILGQTSSQLWLQ 91

Qy         65 LSQSLKGWDHMFTVDFWTIMENHNASK--------ESHTLQVILGCEMQEDNSTEGYWKY 116
              |||||||||:|| ||||||| |:| ||         ||| ||||||||: ||||| |:|||
Db         92 LSQSLKGWDYMFIVDFWTIMGNYNHSKVTKLRVVPESHILQVILGCEVHEDNSTSGFWKY 151

Qy        117 GYDGQDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELG 176
              ||||| |||| ||:| ||||||| ||:||| |:|||||:| ||:|||| ||:|:|||
Db        152 GYDGQDHLEFCPKTLNWSAAEPRAWATKMEWEEHRIRARQSRDYLQRDCPQQLKQVLELQ 211

Qy        177 RGVLDQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLP 236
              |||| |||| ||||| |  |: |:|||:|||::||||||:|||| ||:|||:  |::|||
Db        212 RGVLGQQVPTLVKVTRHWASTGTSLRCQALNFFPQNITMRWLKDSQPLDAKDVNPENVLP 271

Qy        237 NGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||:|||| |||| |::||||||||||||   ||
Db        272 NGDGTYQGWLTLAVAPGEETRFSCQVEHPGLDQPLTATWE 311


RESULT 8
HFE_MOUSE
ID   HFE_MOUSE      STANDARD;      PRT;   359 AA.
AC   P70387;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hereditary hemochromatosis protein homolog precursor.
GN   HFE OR MR2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ;
RX   MEDLINE=98060831; PubMed=9396865;
RA   Riegert P., Gilfillan S., Nanda I., Schmid M., Bahram S.;
RT   "The mouse HFE gene.";
RL   Immunogenetics 47:174-177(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Lung;
RA   Hashimoto K.;
RL   Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 37-211 FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Liver;
RX   MEDLINE=97148566; PubMed=9020055;
RA   Hashimoto K., Hirai M., Kurosawa Y.;
RT   "Identification of a mouse homolog for the human hereditary
RT   haemochromatosis candidate gene.";
RL   Biochem. Biophys. Res. Commun. 230:35-39(1997).
RN   [4]
RP   SEQUENCE OF 79-359 FROM N.A.
RC   STRAIN=129;
RA   Albig W., Drabent B., Doenecke D.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Binds to transferrin receptor (TFR) and reduces its
CC       affinity for iron-loaded transferrin (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: TO MHC CLASS I ANTIGENS.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF007558; AAC03447.1; -.
DR   EMBL; U66849; AAB07525.1; -.
DR   EMBL; Y12650; CAA73197.1; -.
DR   EMBL; U80604; AAB51504.1; -.
DR   PIR; JC5382; JC5382.
DR   HSSP; Q30201; 1A6Z.
DR   MGD; MGI:109191; Hfe.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    359       HEREDITARY HEMOCHROMATOSIS PROTEIN
FT                                 HOMOLOG.
FT   DOMAIN        25    126       EXTRACELLULAR ALPHA-1.
FT   DOMAIN       127    217       EXTRACELLULAR ALPHA-2.
FT   DOMAIN       218    309       EXTRACELLULAR ALPHA-3.
FT   DOMAIN       310    318       CONNECTING PEPTIDE.
FT   TRANSMEM     319    339       POTENTIAL.
FT   DOMAIN       340    359       CYTOPLASMIC TAIL.
FT   DISULFID     136    199       BY SIMILARITY.
FT   DISULFID     237    294       BY SIMILARITY.
FT   CARBOHYD     114    114       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     142    142       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     166    166       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     246    246       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   359 AA;  40548 MW;  4BDE6C27F9FF20B4 CRC64;
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  Query Match             74.6%;  Score 1129;  DB 1;  Length 359;
  Best Local Similarity   71.9%;  Pred. No. 8e-86;
  Matches  202;  Conservative   30;  Mismatches   41;  Indels    8;  Gaps    1;

Qy          4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWL 63
              ||||| |||||||| |||| |||| |||||||| |:||||| ||| ||:  : |||:||
Db         30 RSHSLRYLFMGASEPDLGLPLFEARGYVDDQLFVSYNHESRRAEPRAPWILEQTSSQLWL 89

Qy         64 QLSQSLKGWDHMFTVDFWTIMENHNASK--------ESHTLQVILGCEMQEDNSTEGYWK 115
              |||||||||:|| ||||||| |:| ||         ||| |||:|||| ||||| |:|:
Db         90 HLSQSLKGWDYMFIVDFWTIMGNYNHSKVTKLGVVSESHILQVVLGCEVHEDNSTSGFWR 149

Qy        116 YGYDGQDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLEL 175
              ||||||| ||||| ||:| |||| || ||:||: |||||:||| |||:||| ||::||||
Db        150 YGYDGQDHLEFCPKTLNWSAAEPGAWATKVEWDEHKIRAKQNRDYLEKDCPEQLKRLLEL 209

Qy        176 GRGVLDQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVL 235
              ||||| |||| ||||| |  |: |:|||:||:::|||||:|||| ||:|||:  |: ||
Db        210 GRGVLGQQVPTLVKVTRHWASTGTSLRCQALDFFPQNITMRWLKDNQPLDAKDVNPEKVL 269

Qy        236 PNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||| |||||:||| ||:| |:||||||||||||   ||
Db        270 PNGDETYQGWLTLAVAPGDETRFTCQVEHPGLDQPLTASWE 310
```

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RESULT 9
HA1A_RABIT
ID   HA1A_RABIT     STANDARD;      PRT;   361 AA.
AC   P01894;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   RLA class I histocompatibility antigen, alpha chain 11/11 precursor.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84290724; PubMed=6432910;
RA   Tykocinski M.L., Marche P.N., Max E.E., Kindt T.J.;
RT   "Rabbit class I MHC genes: cDNA clones define full-length transcripts
RT   of an expressed gene and a putative pseudogene.";
RL   J. Immunol. 133:2261-2269(1984).
CC   -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC       immune system.
CC   -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC       microglobulin).
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; K02441; AAA98729.1; -.
DR   PIR; A02193; HLRB.
DR   HSSP; Q30201; 1A6Z.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    361       RLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT                                 ALPHA CHAIN 11/11.
FT   DOMAIN        25    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN       115    206       EXTRACELLULAR ALPHA-2.
FT   DOMAIN       207    298       EXTRACELLULAR ALPHA-3.
FT   DOMAIN       299    308       CONNECTING PEPTIDE.
FT   TRANSMEM     309    329
FT   DOMAIN       330    361       CYTOPLASMIC.
FT   CARBOHYD     110    110       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   DISULFID     125    188       BY SIMILARITY.
FT   DISULFID     227    283       BY SIMILARITY.
SQ   SEQUENCE   361 AA;  40447 MW;  580B673323C1AE35 CRC64;
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  Query Match             34.1%;  Score 517;  DB 1;  Length 361;
  Best Local Similarity   40.1%;  Pred. No. 2.1e-35;
  Matches  111;  Conservative   43;  Mismatches  115;  Indels    8;  Gaps    7;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | :   |   ||   |  :||||| || :| :  | |:| | ||:  ::  : |
Db         26 SHSMRYFYTSVSRPGLGEPRFIIVGYVDDTQFVRFDSDAASPRMEQRAPWM-GQVEPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
              | :|  |    | |:  | :  :| |   ||| | : |||:  |      || :| |||
Db         85 DQQTQIAKDTAQTFRVNLNTALRYYNQSAAGSHTFQTMFGCEVWADGRFFHGYRQYAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
               | :    |   | ||:  |  |: :||     | ::||||||:|   |:: ||:|:  |
Db        145 ADYIALNEDLRSWTAADTAAQNTQRKWEAAG-EAERHRAYLERECVEWLRRYLEMGKETL 203

Qy        181 DQQVPPLVKVTHHVTSS-VTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :  ||   |||| |    |||| || :||  |:: | :| :    :: |  :  | ||
Db        204 QRADPPKAHVTHHPASDREATLRCWALGFYPAEISLTWQRDGED-QTQDTELVETRPGGD 262
```

```
Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || ||||||||:|:| || :|| : ||
Db        263 GTFQKWAAVVVPSGEEQRYTCRVQHEGLPEPLTLTWE 299


RESULT 10
HA1B_RABIT
ID   HA1B_RABIT     STANDARD;      PRT;   361 AA.
AC   P06140;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   RLA class I histocompatibility antigen, alpha chain 19-1 precursor.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85103547; PubMed=3917974;
RA   Marche P.N., Tykocinski M.L., Max E.E., Kindt T.J.;
RT   "Structure of a functional rabbit class I MHC gene: similarity to
RT   human class I genes.";
RL   Immunogenetics 21:71-82(1985).
CC   -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC       immune system.
CC   -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC       microglobulin).
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K02819; AAA98730.1; -.
DR   PIR; I46858; I46858.
DR   HSSP; Q30201; 1A6Z.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    361       RLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT                                 ALPHA CHAIN 19-1.
FT   DOMAIN        25    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN       115    206       EXTRACELLULAR ALPHA-2.
FT   DOMAIN       207    298       EXTRACELLULAR ALPHA-3.
FT   DOMAIN       299    308       CONNECTING PEPTIDE.
FT   TRANSMEM     309    329
FT   DOMAIN       330    361       CYTOPLASMIC.
FT   CARBOHYD     110    110       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   DISULFID     125    188       BY SIMILARITY.
FT   DISULFID     227    283       BY SIMILARITY.
SQ   SEQUENCE   361 AA;  40455 MW;  C06FBD8B87ED0546 CRC64;

  Query Match             34.1%;  Score 517;  DB 1;  Length 361;
  Best Local Similarity   40.1%;  Pred. No. 2.1e-35;
  Matches  111;  Conservative   43;  Mismatches  115;  Indels    8;  Gaps    7;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | :   |   ||   |  :|||||  || :| :  | |:| | ||:  ::  : |
Db         26 SHSMRYFYTSVSRPGLGEPRFIIVGYVDDTQFVRFDSDAASPRMEQRAPWM-GQVEPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
              | :|  |     | |:  | :  :| |   ||| | : |||:  |     || :| |||
Db         85 DQQTQIAKDTAQTFRVNLNTALRYYNQSAAGSHTFQTMFGCEVWADGRFFHGYRQYAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
               | :    |  | ||:  |  |: :||     | ::||||||:|   |:: ||:|:  |
Db        145 ADYIALNEDLRSWTAADTAAQNTQRKWEAAG-EAERHRAYLERECVEWLRRYLEMGKETL 203

Qy        181 DQQVPPLVKVTHHVTSS-VTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
               :  ||   ||||  |    |||| || :||  |:: | :| :    :: |  :  | ||
Db        204 QRADPPKAHVTHHPASDREATLRCWALGFYPAEISLTWQRDGED-QTQDTELVETRPGGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || ||||||||:|:| || :|| : ||
Db        263 GTFQKWAAVVVPSGEEQRYTCRVQHEGLPEPLTLTWE 299


RESULT 11
1A01_PANTR
ID   1A01_PANTR     STANDARD;      PRT;   365 AA.
AC   P16209;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   01-APR-1993 (Rel. 25, Last annotation update)
DE   CHLA class I histocompatibility antigen, A-2 alpha chain precursor.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90201944; PubMed=1690682;
RA   Lawlor D.A., Warren E., Ward F.E., Parham P.;
RT   "Comparison of class I MHC alleles in humans and apes.";
RL   Immunol. Rev. 113:147-185(1990).
CC   -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC       immune system.
CC   -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC       microglobulin).
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M30678; AAA87970.1; -.
DR   PIR; I36961; I36961.
DR   HSSP; Q95352; 1HHK.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    365       CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT                                 A-2 ALPHA CHAIN.
FT   DOMAIN        25    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN       115    206       EXTRACELLULAR ALPHA-2.
FT   DOMAIN       207    298       EXTRACELLULAR ALPHA-3.
FT   DOMAIN       299    308       CONNECTING PEPTIDE.
FT   TRANSMEM     309    332
FT   DOMAIN       333    365       CYTOPLASMIC TAIL.
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FT   DISULFID    125    188       BY SIMILARITY.
FT   DISULFID    227    283       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SQ   SEQUENCE   365 AA;  40848 MW;  FC452786BD038D3E CRC64;

  Query Match             33.8%;  Score 511;  DB 1;  Length 365;
  Best Local Similarity   39.7%;  Pred. No. 6.5e-35;
  Matches  110;  Conservative   44;  Mismatches  115;  Indels    8;  Gaps    7;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |   |    | |:|||||  || :| :  |:|:||| ||:      : |
Db         26 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
               : ::| |       ||  |:   :| |:: |||:|:: ||::  |     || :  |||
Db         85 DEETRSAKAHSQTDRVDLGTLRGYYNQSEDGSHTIQIMYGCDVGSDGRFLRGYRQDAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| :    |   | ||:  |  || :||     | | |||||  |   |:: || |:  |
Db        145 KDYIALNEDLRSWTAADMAAQITKRKWEAAH-AAEQRRAYLEGTCVEWLRRYLENGKETL 203

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :  ||   :||| ::    |||| || :||  ||: | :| :    :: |  :  | ||
Db        204 QRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGED-QTQDTELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  :  || |||||||| |:| || :|| : ||
Db        263 GTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE 299


RESULT 12
HA1B_BOVIN
ID   HA1B_BOVIN     STANDARD;      PRT;   364 AA.
AC   P13753;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   BOLA class I histocompatibility antigen, alpha chain BL3-7 precursor.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88258075; PubMed=3133413;
RA   Ennis P.D., Jackson A.P., Parham P.;
RT   "Molecular cloning of bovine class I MHC cDNA.";
RL   J. Immunol. 141:642-651(1988).
CC   -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC       immune system.
CC   -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC       microglobulin).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M21043; AAA30641.1; -.
DR   HSSP; P16391; 1ED3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     27
FT   CHAIN        28    364       BOLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT                                 ALPHA CHAIN BL3-7.
FT   DOMAIN       28    117       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      118    209       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      210    301       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      302    310       CONNECTING PEPTIDE.
FT   TRANSMEM    311    331
FT   DOMAIN      332    364       CYTOPLASMIC.
FT   CARBOHYD    106    106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    113    113       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   DISULFID    128    191       BY SIMILARITY.
FT   DISULFID    230    286       BY SIMILARITY.
SQ   SEQUENCE   364 AA;  41513 MW;  622056CF7DCF7873 CRC64;

  Query Match             33.7%;  Score 510;  DB 1;  Length 364;
  Best Local Similarity   38.9%;  Pred. No. 7.8e-35;
  Matches  109;  Conservative   49;  Mismatches  114;  Indels    8;  Gaps    7;

Qy          2 LLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISS 59
              |  |||| | : | |   ||   | |:|||||  || :| :  : | ||| ||:
Db         26 LAGSHSLRYFYTGVSRPGLGEPRFIAVGYVDDTQFVRFDSDAPNPREEPRVPWMEQE-GP 84

Qy         60 QMWLQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYG 117
              : | : ::   |    :| ||  |:   :| |:  || :| : ||::  |     |:|::|
Db         85 EYWDRNTRIYKDTAQIFRVDLNTLRGYYNQSETGSHNIQAMYGCDVGPDGRLLRGFWQFG 144

Qy        118 YDGQDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGR 177
              |||:| :    :   | ||:  |  || :||     |   | ||| :|   |:: || |:
Db        145 YDGRDYIALNEELRSWTAADTAAQITKRKWEAAG-AAETWRNYLEGECVEWLRRYLENGK 203

Qy        178 GVLDQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLP 236
              | :  ||   |||| ::    |||| || :||: |:: | :: :    :: |  :  |
Db        204 DTLLRADPPKAHVTHHSISDREVTLRCWALGFYPEEISLTWQREGED-QTQDMELVETRP 262

Qy        237 NGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              :||||:| |  | || ||||||||:|:| || :|| : ||
Db        263 SGDGTFQKWAALVVPSGEEQRYTCRVQHEGLQEPLTLRWE 302


RESULT 13
1A11_HUMAN
ID   1A11_HUMAN     STANDARD;      PRT;   365 AA.
AC   P13746; O19605; O19606; Q29747; Q29835; Q9BCN0; Q9MYI5; Q9TQE9;
AC   Q9TQP6; Q9TQP7;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   HLA class I histocompatibility antigen, A-11 alpha chain precursor
DE   (MHC class I antigen A*11).
GN   HLA-A OR HLAA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (A*1101 AND A*1102).
RX   MEDLINE=89030641; PubMed=2460344;
RA   Mayer W.E., Jonker M., Klein D., Ivanyi P., van Seventer G.,
RA   Klein J.;
RT   "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
RT   trans-species mode of evolution.";
RL   EMBO J. 7:2765-2774(1988).
RN   [2]
RP   SEQUENCE FROM N.A. (A*1101 AND A*1102).
RX   MEDLINE=94287401; PubMed=8016845;
RA   Lin L., Tokunaga K., Ishikawa Y., Bannai M., Kashiwase K.,
RA   Kuwata S., Akaza T., Tadokoro K., Shibata Y., Juji T.;
RT   "Sequence analysis of serological HLA-A11 split antigens, A11.1 and
RT   A11.2.";
```

```
RL   Tissue Antigens 43:78-82(1994).
RN   [3]
RP   SEQUENCE OF 26-365 FROM N.A. (A*1101).
RX   MEDLINE=87192928; PubMed=2437024;
RA   Cowan E.P., Jelachich M.L., Biddison W.E., Coligan J.E.;
RT   "DNA sequence of HLA-A11: remarkable homology with HLA-A3 allows
RT   identification of residues involved in epitopes recognized by
RT   antibodies and T cells.";
RL   Immunogenetics 25:241-250(1987).
RN   [4]
RP   SEQUENCE FROM N.A. (A*1103).
RC   TISSUE=Blood;
RX   MEDLINE=20166353; PubMed=10703613;
RA   Tijssen H.J., Sistermans E.A., van den Beucken M.J.G., Krausa P.,
RA   Joosten I.;
RT   "Complete sequence analysis of the A*1103 allele.";
RL   Tissue Antigens 55:68-70(2000).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 2) (A*1103).
RC   TISSUE=Blood;
RX   MEDLINE=20340071; PubMed=10885562;
RA   Tijssen H.J., Sistermans E.A., Joosten I.;
RT   "A unique second donor splice site in the intron 5 sequence of the
RT   HLA-A*11 alleles results in a class I transcript encoding a molecule
RT   with an elongated cytoplasmic domain.";
RL   Tissue Antigens 55:422-428(2000).
RN   [6]
RP   SEQUENCE FROM N.A. (A*1104).
RA   Bettinotti M.P.;
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE OF 26-206 FROM N.A. (A*1104).
RA   Chandanayingyong D., Sirikong M., Luangtrakool K., Srinak D.,
RA   Rungroung E., Bejchandra S.;
RT   "A11 alleles (A*1104).";
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   SEQUENCE FROM N.A. (A*1105).
RX   MEDLINE=99321035; PubMed=10395112;
RA   Morrell G., Whalley J., Stewart A., Day S., Lewis L., Makar Y.,
RA   Ross J., Dunn P.P.;
RT   "Identification of an HLA-A11 serological variant and its
RT   characterization by sequencing based typing.";
RL   Tissue Antigens 53:591-594(1999).
RN   [9]
RP   SEQUENCE OF 26-206 FROM N.A. (A*1105).
RX   MEDLINE=20309230; PubMed=10852390;
RA   Ellis J., Steiner N.K., Kosman C., Henson V., Mitton W., Koester R.,
RA   Ng J., Hartzman R.J., Hurley C.K.;
RT   "Seventeen more novel HLA-A locus alleles.";
RL   Tissue Antigens 55:369-373(2000).
RN   [10]
RP   SEQUENCE FROM N.A. (A*1107).
RX   MEDLINE=21561663; PubMed=11703829;
RA   Pyo C.W., Choi H.B., Han H., Hong Y.S., Kim T.G.;
RT   "Identification of HLA-A*11 variant (A*1107) in the Korean
RT   population.";
RL   Tissue Antigens 58:190-192(2001).
CC   -!- FUNCTION: Involved in the presentation of foreign antigens to
CC       the immune system.
CC   -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC       microglobulin).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=P13746-1; Sequence=Displayed;
CC       Name=2; Synonyms=Long;
CC         IsoId=P13746-2; Sequence=VSP_008099;
CC         Note=Only produced by allele A*1103;
CC   -!- POLYMORPHISM: The following alleles of A-11 are known: A*1101
CC       (A-11E), A*1102 (A-11K), A*1103, A*1104, A*1105 and A*1107. The
CC       sequence shown is that of A*1101.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X13111; CAA31503.1; -.
DR   EMBL; X13112; CAA31504.1; -.
DR   EMBL; D16841; BAA04117.1; -.
DR   EMBL; D16842; BAA04118.1; -.
DR   EMBL; M16010; AAA65449.1; -.
DR   EMBL; M16007; AAA65449.1; JOINED.
DR   EMBL; M16008; AAA65449.1; JOINED.
DR   EMBL; M16009; AAA65449.1; JOINED.
DR   EMBL; Y17224; CAB38056.1; -.
DR   EMBL; Y17224; CAB38057.1; -.
DR   EMBL; X91399; CAA62745.1; -.
DR   EMBL; U50574; AAB60406.1; -.
DR   EMBL; AF030910; AAB87052.1; -.
DR   EMBL; AF030909; AAB87052.1; JOINED.
DR   EMBL; AF030908; AAB87051.1; -.
DR   EMBL; AF030907; AAB87051.1; JOINED.
DR   EMBL; AJ306733; CAC37336.1; -.
DR   EMBL; AF147455; AAD33991.1; -.
DR   EMBL; AF147454; AAD33991.1; JOINED.
DR   EMBL; AF165065; AAF25781.1; -.
DR   PIR; I83063; I83063.
DR   PIR; S03536; A47636.
DR   HSSP; O19673; 1HSB.
DR   Genew; HGNC:4931; HLA-A.
DR   MIM; 142800; -.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0030106; F:MHC class I receptor activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   MHC I; Signal; Transmembrane; Glycoprotein; Alternative splicing;
KW   Polymorphism.
FT   SIGNAL       1     24
FT   CHAIN       25    365       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT                                A-11 ALPHA CHAIN.
FT   DOMAIN      25    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN     115    206       EXTRACELLULAR ALPHA-2.
FT   DOMAIN     207    298       EXTRACELLULAR ALPHA-3.
FT   DOMAIN     299    308       CONNECTING PEPTIDE.
FT   TRANSMEM   309    332
FT   DOMAIN     333    365       CYTOPLASMIC TAIL.
FT   CARBOHYD   110    110       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   DISULFID   125    188       BY SIMILARITY.
FT   DISULFID   227    283       BY SIMILARITY.
FT   VARSPLIC   337    337       S -> SGGEGVK (in isoform 2).
FT                               /FTId=VSP_008099.
FT   VARIANT     43     43       E -> K (in allele A*1102).
FT                               /FTId=VAR_004353.
FT   VARIANT    133    133       F -> L (in allele A*1107).
FT                               /FTId=VAR_016731.
FT   VARIANT    168    168       K -> E (in allele A*1105).
FT                               /FTId=VAR_016732.
FT   VARIANT    175    175       H -> R (in allele A*1103).
FT                               /FTId=VAR_016733.
FT   VARIANT    176    176       A -> E (in allele A*1103).
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FT                                /FTId=VAR_016734.
FT   VARIANT     187    187       R -> T (in allele A*1104).
FT                                /FTId=VAR_016735.
FT   VARIANT     345    345       T -> S (in allele A*1105).
FT                                /FTId=VAR_016736.
SQ   SEQUENCE   365 AA;  40937 MW;  FE449CE2D4BF6CC5 CRC64;

  Query Match             33.6%;  Score 508;  DB 1;  Length 365;
  Best Local Similarity   39.4%;  Pred. No. 1.1e-34;
  Matches  109;  Conservative   46;  Mismatches  114;  Indels    8;  Gaps    7;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | :   |    |   | |:|||||  || :| :  :|:|:||| ||:      : |
Db         26 SHSMRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
               | ::::|       ||  |:   :| |:: |||:|:: ||::  |     || :  |||
Db         85 DQETRNVKAQSQTDRVDLGTLRGYYNQSEDGSHTIQIMYGCDVGPDGRFLRGYRQDAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| :   |   | ||:  |  || :||     | | |||||  |   |:: || |: |
Db        145 KDYIALNEDLRSWTAADMAAQITKRKWEAAH-AAEQQRAYLEGRCVEWLRRYLENGKETL 203

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
               :  ||   :||| ::    |||| || :||  ||: | :| :    :: |  :  | ||
Db        204 QRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGED-QTQDTELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |||||||| |:| || :|| : ||
Db        263 GTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE 299
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RESULT 14
1A03_HUMAN
ID   1A03_HUMAN     STANDARD;      PRT;   365 AA.
AC   P04439; O19546; O19756; Q9GJE6; Q9GJE7; Q9GJE8; Q9MYG4; Q9TPR8;
DT   13-AUG-1987 (Rel. 05, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   HLA class I histocompatibility antigen, A-3 alpha chain precursor
DE   (MHC class I antigen A*3).
GN   HLA-A OR HLAA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (A*0301).
RX   MEDLINE=84207948; PubMed=6609814;
RA   Strachan T., Sodoyer R., Damotte M., Jordan B.R.;
RT   "Complete nucleotide sequence of a functional class I HLA gene,
RT   HLA-A3: implications for the evolution of HLA genes.";
RL   EMBO J. 3:887-894(1984).
RN   [2]
RP   SEQUENCE FROM N.A. (A*0301).
RA   Ellexson M.E., Hildebrand W.H.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (A*0301).
RA   Shiina S., Tamiya G., Oka A., Inoko H.;
RT   "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (A*0302).
RX   MEDLINE=85290871; PubMed=2993417;
RA   Cowan E.P., Jordan B.E., Coligan J.E.;
RT   "Molecular cloning and DNA sequence analysis of genes encoding
RT   cytotoxic T lymphocyte-defined HLA-A3 subtypes: the E1 subtype.";
RL   J. Immunol. 135:2835-2841(1985).
RN   [5]
RP   SEQUENCE FROM N.A. (A*0302).
RA   Bettinotti M.P., Hadzikadic L., Adams S., Marincola F.M.;
RT   "Complete coding sequence of HLA-A*0302.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE OF 1-341 FROM N.A. (A*0304).
RX   MEDLINE=99180630; PubMed=10079303;
RA   Santos S., Balas A., Garcia-Sanchez F., Lillo R., Merino J.L.,
RA   Vicario J.L.;
RT   "Complete cDNA coding sequence of a new HLA-A3 subtype (A*0304) with a
RT   new HLA polymorphism at exon 3.";
RL   Immunogenetics 49:360-361(1999).
RN   [7]
RP   SEQUENCE OF 26-206 FROM N.A. (A*0305).
RA   Becher M.P., Wu J., Williams T.;
RT   "Novel human HLA-A alleles identified in potential bone marrow
RT   donors.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   SEQUENCE OF 26-298 FROM N.A. (A*0305).
RC   TISSUE=Blood;
RA   Poli F., Frison S., Crespiatico L., Longhi E.;
RT   "Identification of a HLA-A*03 new variant.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Involved in the presentation of foreign antigens to
CC       the immune system.
CC   -!- SUBUNIT: Dimer of alpha chain and a beta chain (beta-2-
CC       microglobulin).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- POLYMORPHISM: The following alleles of A-3 are known: A*0301
CC       (A-3.1), A*0302, A*0304 and A*0305. The sequence shown is that of
CC       A*0301.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X00492; CAA25162.1; ALT_SEQ.
DR   EMBL; U32184; AAB63980.1; -.
DR   EMBL; AP000520; BAB63400.1; -.
DR   EMBL; AP000519; BAB63400.1; JOINED.
DR   EMBL; AF217561; AAF28734.1; -.
DR   EMBL; AF015930; AAB66582.1; -.
DR   EMBL; AF190719; AAF03243.1; -.
DR   EMBL; AF190718; AAF03243.1; JOINED.
DR   EMBL; AJ401085; CAC06086.1; -.
DR   EMBL; AJ401086; CAC06087.1; -.
DR   EMBL; AJ401087; CAC06088.1; -.
DR   PIR; A02192; HLHUA3.
DR   HSSP; O19673; 1HSB.
DR   Genew; HGNC:4931; HLA-A.
DR   MIM; 142800; -.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0030106; F:MHC class I receptor activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
FT   SIGNAL        1     24
FT   CHAIN        25    365       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT                                 A-3 ALPHA CHAIN.
FT   DOMAIN       25    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      115    206       EXTRACELLULAR ALPHA-2.
```

```
FT   DOMAIN      207    298       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      299    308       CONNECTING PEPTIDE.
FT   TRANSMEM    309    332
FT   DOMAIN      333    365       CYTOPLASMIC TAIL.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   DISULFID    125    188       BY SIMILARITY.
FT   DISULFID    227    283       BY SIMILARITY.
FT   VARIANT     176    176       E -> V (in allele A*0302).
FT                                /FTId=VAR_004351.
FT   VARIANT     180    180       L -> Q (in allele A*0302).
FT                                /FTId=VAR_004352.
FT   VARIANT     185    185       D -> E (in allele A*0305).
FT                                /FTId=VAR_016604.
FT   VARIANT     199    199       G -> R (in allele A*0304).
FT                                /FTId=VAR_016605.
FT   CONFLICT    319    319       G -> A (IN REF. 6).
SQ   SEQUENCE   365 AA;  40840 MW;  DEDFCEC4450E0580 CRC64;

  Query Match             33.4%;  Score 506;  DB 1;  Length 365;
  Best Local Similarity   39.6%;  Pred. No. 1.7e-34;
  Matches  110;  Conservative   46;  Mismatches  112;  Indels   10;  Gaps    8;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |     |   | |:|||||   || :| :  |:|:||| ||:      : |
Db         26 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
               | ::::|        ||  |:   :| |:  |||:|:: ||::  |      || :  |||
Db         85 DQETRNVKAQSQTDRVDLGTLRGYYNQSEAGSHTIQIMYGCDVGSDGRFLRGYRQDAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWE-RHKIRARQNRAYLERDCPAQLQQLLELGRGV 179
              :| :     |   | ||:  |   || :||  |:  | | ||||:  |    |:: || |:
Db        145 KDYIALNEDLRSWTAADMAAQITKRKWEAAHE--AEQLRAYLDGTCVEWLRRYLENGKET 202

Qy        180 LDQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNG 238
              | :  ||   :||| ::    |||| || :||  ||: | :| :     :: |  :  | |
Db        203 LQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGED-QTQDTELVETRPAG 261

Qy        239 DGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||:| |   : || |||||||| |:| || :|| : ||
Db        262 DGTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE 299


RESULT 15
1A80_HUMAN
ID   1A80_HUMAN     STANDARD;      PRT;   365 AA.
AC   Q09160;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   HLA class I histocompatibility antigen, A-80 alpha chain precursor
DE   (MHC class I antigen A*80) (Aw-80) (A-1).
GN   HLA-A OR HLAA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (A*8001).
RX   MEDLINE=94245293; PubMed=8188325;
RA   Balas A., Garcia-Sanchez F., Gomez-Reino F., Vicario J.L.;
RT   "Characterization of a new and highly distinguishable HLA-A allele in
RT   a Spanish family.";
RL   Immunogenetics 39:452-452(1994).
RN   [2]
RP   SEQUENCE FROM N.A. (A*8001).
RA   Domena J.D.;
RL   Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC       immune system.
CC   -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC       microglobulin).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- POLYMORPHISM: The only allele of A-80 known is A*8001 which is
CC       shown here.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U03754; AAC04322.1; -.
DR   EMBL; L18898; AAA17012.1; -.
DR   PIR; I59638; I38439.
DR   HSSP; Q95352; 1HHK.
DR   Genew; HGNC:4931; HLA-A.
DR   MIM; 142800; -.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0030106; F:MHC class I receptor activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    365       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT                                A-80 ALPHA CHAIN.
FT   DOMAIN       25    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      115    206       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      207    298       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      299    308       CONNECTING PEPTIDE.
FT   TRANSMEM    309    332
FT   DOMAIN      333    365       CYTOPLASMIC TAIL.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   DISULFID    125    188       BY SIMILARITY.
FT   DISULFID    227    283       BY SIMILARITY.
SQ   SEQUENCE   365 AA;  40791 MW;  CE1BC1CD60CA8FA8 CRC64;

  Query Match             33.3%;  Score 504;  DB 1;  Length 365;
  Best Local Similarity   38.3%;  Pred. No. 2.5e-34;
  Matches  106;  Conservative   52;  Mismatches  111;  Indels    8;  Gaps    7;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |     |   | |:|||||   || :| :  |:|:||| ||:      : |
Db         26 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDSQFVQFDSDAASQRMEPRAPWIEQE-EPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
               : ::::|       :  |:   :| |:: |||:|:: ||::  |      || :  |||
Db         85 DEETRNVKAHSQTNRANLGTLRGYYNQSEDGSHTIQIMYGCDVGSDGRFLRGYRQDAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| :     |   | ||:  |   || :||  : || | ||||| :|   |:: || |:  |
Db        145 KDYIALNEDLRSWTAADMAAQITKRKWEAAR-RAEQLRAYLEGECVDGLRRYLENGKETL 203

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :  ||   :||| ::    ||||  ||::||   ||: | :| :    :: |  :  | ||
Db        204 QRTDPPKTHMTHHPISDHEATLRCWALSFYPAEITLTWQRDGED-QTQDTELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |   : || |:|:|||| |:| || :|| : ||
Db        263 GTFQKWAAVVVPSGKEKRYTCHVQHEGLPEPLTLRWE 299


Search completed: May  4, 2004, 11:35:41
Job time : 9.33333 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 4, 2004, 11:32:18 ; Search time 34.6667 Seconds
(without alignments)
2512.010 Million cell updates/sec

Title: US-10-092-404-3
Perfect score: 1514
Sequence: 1 RLLRSHSLHYLFMGASEQDL.....RYTCQVEHPGLDQPLIVIWE 276

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1200	79.3	268	4	Q86WL1	Q86wl1 homo sapien
2	1129	74.6	358	11	Q8C2A6	Q8c2a6 mus musculu
3	1129	74.6	359	11	Q9D754	Q9d754 mus musculu
4	792	52.3	272	11	Q9R105	Q9r105 rattus norv
5	574	37.9	116	4	Q9HC69	Q9hc69 homo sapien
6	540.5	35.7	359	7	Q8HX81	Q8hx81 ornithorhyn
7	537.5	35.5	354	7	Q95HB3	Q95hb3 anas platyr
8	531.5	35.1	340	7	Q9BD50	Q9bd50 pongo pygma
9	530.5	35.0	334	7	Q9TQK3	Q9tqk3 homo sapien
10	530.5	35.0	341	4	Q9NPL2	Q9npl2 homo sapien
11	530.5	35.0	341	7	Q95460	Q95460 homo sapien
12	530.5	35.0	341	7	Q9BCU3	Q9bcu3 pan troglod
13	527.5	34.8	341	7	Q9BCU4	Q9bcu4 pan troglod
14	515	34.0	356	7	Q8HX66	Q8hx66 sus scrofa
15	514	33.9	332	7	Q30990	Q30990 pan troglod
16	514	33.9	365	7	Q9TPL7	Q9tpl7 pan troglod
17	513	33.9	312	7	Q860B4	Q860b4 homo sapien
18	512	33.8	105	4	Q9HC71	Q9hc71 homo sapien
19	512	33.8	129	4	Q9UK37	Q9uk37 homo sapien
20	511	33.8	352	7	Q8MHT1	Q8mht1 sus scrofa
21	511	33.8	364	7	O19243	O19243 sus scrofa
22	508	33.6	273	7	Q95IG6	Q95ig6 homo sapien
23	508	33.6	352	7	Q8SPA9	Q8spa9 sus scrofa
24	508	33.6	361	7	Q8HX63	Q8hx63 sus scrofa
25	508	33.6	364	7	Q8HX61	Q8hx61 sus scrofa
26	507	33.5	91	4	Q9BXI5	Q9bxi5 homo sapien
27	507	33.5	91	7	Q8MH46	Q8mh46 homo sapien
28	507	33.5	330	7	O19356	O19356 macaca mula
29	507	33.5	331	7	O02944	O02944 macaca mula
30	507	33.5	333	7	O98030	O98030 papio anubi
31	507	33.5	333	7	O98031	O98031 papio anubi
32	506	33.4	330	7	O02947	O02947 macaca mula
33	506	33.4	330	7	O02946	O02946 macaca mula
34	505	33.4	331	7	O02945	O02945 macaca mula
35	505	33.4	357	7	Q30886	Q30886 pan paniscu
36	505	33.4	363	7	Q9MXI5	Q9mxi5 pan troglod
37	505	33.4	363	7	Q9MWK4	Q9mwk4 gorilla gor
38	505	33.4	365	7	Q9MXI6	Q9mxi6 pan troglod
39	505	33.4	365	7	Q9MXM7	Q9mxm7 pan troglod
40	504	33.3	360	7	Q9GJ24	Q9gj24 homo sapien
41	504	33.3	364	7	Q8SPA4	Q8spa4 sus scrofa
42	504	33.3	365	7	Q30900	Q30900 pan paniscu
43	504	33.3	365	7	Q8HWQ9	Q8hwq9 homo sapien
44	503.5	33.3	360	7	Q95558	Q95558 peromyscus
45	503	33.2	273	7	Q9TQP8	Q9tqp8 homo sapien

ALIGNMENTS

RESULT 1
Q86WL1
ID Q86WL1 PRELIMINARY; PRT; 268 AA.
AC Q86WL1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hemochromatosis (Fragment).
GN HFE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kutlar F., Nechtman J., Leithner C.;
RT "Direct isolation of hemochromatosis (HFE) mRNA from the whole blood
RT of a normal Caucasian individual.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY205604; AAO47091.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1 1
SQ SEQUENCE 268 AA; 30952 MW; D725DE42AC08DAA5 CRC64;

Query Match 79.3%; Score 1200; DB 4; Length 268;
Best Local Similarity 99.1%; Pred. No. 3.8e-104;
Matches 216; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          59 SQMWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGY 118
               ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db           1 SQMWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGY 60

Qy         119 DGQDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRG 178
               |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DGQDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRG 120

Qy         179 VLDQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNG 238
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 VLDQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNG 180

Qy         239 DGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
               |||||||||||||||||||||||||||||||||||||
Db         181 DGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 218
```

RESULT 2
Q8C2A6
ID Q8C2A6 PRELIMINARY; PRT; 358 AA.
AC Q8C2A6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hemochromatosis.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK088986; BAC40688.1; -.
DR PIR; PT0706; PT0706.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 358 AA; 40421 MW; EE88FB6E5AAC844D CRC64;

Query Match 74.6%; Score 1129; DB 11; Length 358;
Best Local Similarity 71.9%; Pred. No. 2.4e-97;
Matches 202; Conservative 30; Mismatches 41; Indels 8; Gaps 1;

```
Qy           4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWL 63
               ||||| |||||||| |||| |||| ||||||||| |:||||| ||| ||:  : |||:||
Db          29 RSHSLRYLFMGASEPDLGLPLFEARGYVDDQLFVSYNHESRRAEPRAPWILEQTSSQLWL 88

Qy          64 QLSQSLKGWDHMFTVDFWTIMENHNASK--------ESHTLQVILGCEMQEDNSTEGYWK 115
               |||||||||:|| ||||||| |:| ||         ||| |||:|||| ||||| |:|:
Db          89 HLSQSLKGWDYMFIVDFWTIMGNYNHSKVTKLGVVSESHILQVVLGCEVHEDNSTSGFWR 148

Qy         116 YGYDGQDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLEL 175
               ||||||| ||||| ||:| |||| || ||:||: |||||:||| |||:||| ||::||||
Db         149 YGYDGQDHLEFCPKTLNWSAAEPGAWATKVEWDEHKIRAKQNRDYLEKDCPEQLKRLLEL 208

Qy         176 GRGVLDQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVL 235
               ||||| |||| ||||| |  |: |:|||:||:::|||||:|||| ||:|||:  |: ||
```

```
Db         209 GRGVLGQQVPTLVKVTRHWASTGTSLRCQALDFFPQNITMRWLKDNQPLDAKDVNPEKVL 268

Qy         236 PNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
               |||| ||||:|||| ||:| |:|||||||||||   ||
Db         269 PNGDETYQGWLTLAVAPGDETRFTCQVEHPGLDQPLTASWE 309
```

RESULT 3
Q9D754
ID Q9D754 PRELIMINARY; PRT; 359 AA.
AC Q9D754;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adult male tongue cDNA, RIKEN full-length enriched library,
DE clone:2310032M04, full insert sequence.
GN HFE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL; AK009581; BAB26373.1; -.
DR HSSP; Q30201; 1A6Z.
DR MGD; MGI:109191; Hfe.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
SQ SEQUENCE 359 AA; 40534 MW; 586657B7F9FF20B4 CRC64;

Query Match 74.6%; Score 1129; DB 11; Length 359;
Best Local Similarity 71.9%; Pred. No. 2.4e-97;
Matches 202; Conservative 30; Mismatches 41; Indels 8; Gaps 1;

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Qy           4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWL 63
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                |||||  |||||||| |||| |||| |||||||||  |:|||||  ||| ||:  : |||:||
Db          30 RSHSLRYLFMGASEPDLGLPLFEARGYVDDQLFVSYNHESRRAEPRAPWILEQTSSQLWL 89

Qy          64 QLSQSLKGWDHMFTVDFWTIMENHNASK--------ESHTLQVILGCEMQEDNSTEGYWK 115
               |||||||||:|| |||||||  |:| ||         ||| |||:|||: |||||  |:|:
Db          90 HLSQSLKGWDYMFIVDFWTIMGNYNHSKVTKLGVVSESHILQVVLGCEVHEDNSTSGFWR 149

Qy         116 YGYDGQDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLEL 175
               |||||||  |||||  ||:|  ||||  ||  ||:||:  |||||:|||  |||:|||  ||::||||
Db         150 YGYDGQDHLEFCPKTLNWSAAEPGAWATKVEWDEHKIRAKQNRDYLEKDCPEQLKRLLEL 209

Qy         176 GRGVLDQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVL 235
               |||||  ||||  |||||  |  |:  |:|||:||:::||||||:|||| ||:|||:  |: ||
Db         210 GRGVLGQQVPTLVKVTRHWASTGTSLRCQALDFFPQNITMRWLKDNQPLDAKDVNPEKVL 269

Qy         236 PNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
               ||||  |||||:|||| ||:| |:|||||||||||||    ||
Db         270 PNGDETYQGWLTLAVAPGDETRFTCQVEHPGLDQPLTASWE 310


RESULT 4
Q9R105
ID   Q9R105      PRELIMINARY;      PRT;   272 AA.
AC   Q9R105;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hemochromatosis gene product HFE splice variant delE2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Testis;
RA   Liew Y.-F., Shaw N.-S.;
RT   "Alternative splice variant of the hemochromatosis gene HFE in iron
RT   overloaded rats.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC       IMMUNE SYSTEM (BY SIMILARITY).
CC   -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC       MICROGLOBULIN) (BY SIMILARITY).
DR   EMBL; AF176534; AAD49965.1; -.
DR   HSSP; Q30201; 1A6Z.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Glycoprotein; Transmembrane.
SQ   SEQUENCE   272 AA;  30757 MW;  1D91063CCBEF5502 CRC64;

  Query Match             52.3%;  Score 792;  DB 11;  Length 272;
  Best Local Similarity   74.6%;  Pred. No. 6.2e-66;
  Matches  138;  Conservative   22;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          92 ESHTLQVILGCEMQEDNSTEGYWKYGYDGQDALEFCPDTLDWRAAEPRAWPTKLEWERHK 151
               ||| ||||||||: ||||| |:||||||||| ||||| ||:| ||||||| ||:||| |:
Db          39 ESHILQVILGCEVHEDNSTSGFWKYGYDGQDHLEFCPKTLNWSAAEPRAWATKMEWEEHR 98

Qy         152 IRARQNRAYLERDCPAQLQQLLELGRGVLDQQVPPLVKVTHHVTSSVTTLRCRALNYYPQ 211
               |||||:| ||:|||| ||:|:||| |||| |||| ||||| |  |: |:|||:|||:||
Db          99 IRARQSRDYLQRDCPQQLKQVLELQRGVLGQQVPTLVKVTRHWASTGTSLRCQALNFFPQ 158

Qy         212 NITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPL 271
               ||||:|||| ||:|||:  |::|||||||||||:|||| |||| |::|||||||||||
Db         159 NITMRWLKDSQPLDAKDVNPENVLPNGDGTYQGWLTLAVAPGEETRFSCQVEHPGLDQPL 218

Qy         272 IVIWE 276
                 ||
Db         219 TATWE 223


RESULT 5
Q9HC69
ID   Q9HC69      PRELIMINARY;      PRT;   116 AA.
AC   Q9HC69;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hemochromatosis splice variant 861-2305del (Fragment).
GN   HFE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20448010; PubMed=11001625;
RA   Thenie A., Orhant M., Gicquel I., Fergelot P., Le Gall J.Y., David V.,
RA   Mosser J.;
RT   "The HFE gene undergoes alternate splicing processes.";
RL   Blood Cells Mol. Dis. 26:155-162(2000).
DR   EMBL; AF144241; AAG29576.1; -.
DR   HSSP; Q30201; 1A6Z.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   116 AA;  13541 MW;  AC0333B096A3F47B CRC64;

  Query Match             37.9%;  Score 574;  DB 4;  Length 116;
  Best Local Similarity   98.1%;  Pred. No. 5.6e-46;
  Matches  104;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          90 SKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDALEFCPDTLDWRAAEPRAWPTKLEWER 149
               |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db           2 SKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDHLEFCPDTLDWRAAEPRAWPTKLEWER 61

Qy         150 HKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQVPPLVKVTHHVT 195
               |||||||||||||||||||||||||||||||||||||||||||||:
Db          62 HKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQVPPLVKVTHHVS 107


RESULT 6
Q8HX81
ID   Q8HX81      PRELIMINARY;      PRT;   359 AA.
AC   Q8HX81;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   MHC class I antigen.
OS   Ornithorhynchus anatinus (Duckbill platypus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
OX   NCBI_TaxID=9258;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22226695; PubMed=12242589;
RA   Miska K.B., Harrison G.A., Hellman L., Miller R.D.;
RT   "The major histocompatibility complex in monotremes: an analysis of
RT   the evolution of Mhc class I genes across all three mammalian
RT   subclasses.";
RL   Immunogenetics 54:381-393(2002).
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DR   EMBL; AY112715; AAM54213.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   359 AA;  39847 MW;  3FC701E44FD53B66 CRC64;

  Query Match             35.7%;  Score 540.5;  DB 7;  Length 359;
  Best Local Similarity   40.6%;  Pred. No. 3.2e-42;
  Matches  113;  Conservative   51;  Mismatches  107;  Indels    7;  Gaps    5;

Qy          4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHES--RRVEPRTPWVSSRISSQM 61
              ||||| | : | |    |:| | |:|||:  || :: :    | ||||||:      :
Db         25 RSHSLRYFYTGVSRPGSGVSEFTAVGYVDEVQFVRFEGDGGRGRAEPRTPWIRDNEGQEY 84

Qy         62 WLQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNST-EGYWKYGYD 119
              | : :| ||    :|   :  | :  :| ||| ||| | : ||:::||::  :|: :|||
Db         85 WDRNTQILKDTAQVFRTNLQTALGYYNQSKEGSHTFQRMYGCQLREDDTPGQGFTQYGYD 144

Qy        120 GQDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGV 179
              |:| :     || | ||:  |  || :||  :  | :::|||| :|    |:: :  |
Db        145 GRDYIALDKATLSWTAADAGALNTKRKWEADRTIAERDKAYLEDECIEWLRKYVGFGGPS 204

Qy        180 LDQQVPPLVKVTHHV--TSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPN 237
              | :  || |:|| |         :|||||| :|| :|  || :: : | ::| |      |:
Db        205 LTRADPPEVEVTRHTGPDGEDVSLRCRALGFYPADIKFKWEREGKDM-SQEMEFVGTRPS 263

Qy        238 GDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIW 275
              ||| :| | :: || ||||:| | ||| || ||| | |
Db        264 GDGNFQKWASVNVPRGEEQKYVCVVEHEGLGQPLAVKW 301


RESULT 7
Q95HB3
ID   Q95HB3      PRELIMINARY;      PRT;   354 AA.
AC   Q95HB3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   MHC class I antigen alpha chain (Fragment).
OS   Anas platyrhynchos (Domestic duck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX   NCBI_TaxID=8839;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Chan S.W.S., Middleton D.L., Lundqvist M., Warr G.W., Higgins D.A.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF393511; AAK84356.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   MHC.
FT   NON_TER       1      1
SQ   SEQUENCE   354 AA;  39405 MW;  D44FACEE7B60468F CRC64;

  Query Match             35.5%;  Score 537.5;  DB 7;  Length 354;
  Best Local Similarity   37.3%;  Pred. No. 5.9e-42;
  Matches  101;  Conservative   60;  Mismatches  109;  Indels    1;  Gaps    1;

Qy          6 HSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQL 65
              ||| |      |:   |:  | |:|||| ::|| || |:| :|||  |::  :  | |
Db         24 HSLRYFATAVSDPSPGVPQFVAVGYVDGEVFVRYDSETRGMEPRVDWIADNMDQQYWNGE 83

Qy         66 SQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDALE 125
              :::|:| : :: ||  |: | :| |: ||||| : ||:: || |  |:::|||:|:: :
Db         84 TENLRGAEQIYRVDLETLRERYNQSRGSHTLQHMFGCDLLEDRSISGFFQYGYEGREFIA 143

Qy        126 FCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQVP 185
                ||  : ||:  |  || :||      | : : |||  |   |:: :  |: ||:::
Db        144 LDKDTWTFTAADAAAQITKRKWEEDGTVAERRKYYLENTCIEWLRKYVRYGKDVLERRER 203

Qy        186 PLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGW 245
              | |:|:      : :| |||  :||: |:: |||  :  :| :   :|| ||||  |
Db        204 PEVRVSGMEADKILSLSCRAHGFYPRPISISWLKDGM-VQEQETQRGSTVPNSDGTYHIW 262

Qy        246 ITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |: | ||:: :| |:|||  | || :  ||
Db        263 ATIDVVPGDKDKYQCRVEHASLPQPGLFSWE 293


RESULT 8
Q9BD50
ID   Q9BD50      PRELIMINARY;      PRT;   340 AA.
AC   Q9BD50;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   MHC class I related protein MR1 isoform.
GN   MR1.
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Parra-Cuadrado J.F., Garcia-Pavia P., Gomez del Moral M.,
RA   Martinez-Naves E.;
RT   "Identification of MR1 cDNA sequences in non-human primates.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC       IMMUNE SYSTEM (BY SIMILARITY).
CC   -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC       MICROGLOBULIN) (BY SIMILARITY).
DR   EMBL; AJ271828; CAC28215.1; -.
DR   HSSP; Q30201; 1A6Z.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Glycoprotein; Transmembrane.
SQ   SEQUENCE   340 AA;  39375 MW;  A893952B78725F17 CRC64;

  Query Match             35.1%;  Score 531.5;  DB 7;  Length 340;
  Best Local Similarity   39.1%;  Pred. No. 2e-41;
  Matches  106;  Conservative   51;  Mismatches  111;  Indels    3;  Gaps    3;
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Qy          4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWL 63
              |:||| |  :| |:   |:  | ::||||      ||  ::: ||| ||::  ::   |
Db         23 RTHSLRYFRLGVSDPIRGVPEFISVGYVDSHPITTYDSVTQQKEPRAPWMAENLAPDHWE 82

Qy         64 QLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDA 123
              : :| |:||  || |:   :  ::| |  ||| | ::|||: || || |: :| |||||
Db         83 RYTQLLRGWQQMFKVELKRLQRHYNHS-GSHTYQRMIGCELLEDGSTTGFLQYAYDGQDF 141

Qy        124 LEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQ 183
              | |  ||| | | :  |   |  || ::   :  : :|| :| | |:: || |:  | :
Db        142 LIFNKDTLSWLAVDNVAHTIKRAWEANQHELQYQKNWLEEECIAWLKRFLEYGKDTLQRT 201

Qy        184 VPPLVKVTHHVT-SSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTY 242
               ||||:|    |   |||| |:|  :||  | | |:|: : :  :| :  |:||:|||||
Db        202 EPPLVRVNRKETFPGVTTLFCKAHGFYPPEIYMTWMKNGEEI-VQEMDYGDILPSGDGTY 260

Qy        243 QGWITLAVPPGEEQRYTCQVEHPGLDQPLIV 273
              | | :  : |    |:| ||| |:   | |
Db        261 QTWASFELDPQSSNLYSCHVEHCGVHMVLQV 291


RESULT 9
Q9TQK3
ID   Q9TQK3      PRELIMINARY;      PRT;   334 AA.
AC   Q9TQK3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   MHC class I-related protein MR1 (Fragment).
GN   MR1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=99003494; PubMed=9784382;
RA   Yamaguchi H., Kurosawa Y., Hashimoto K.;
RT   "Expanded genomic organization of conserved mammalian MHC class I-
RT   related genes, human MR1 and its murine ortholog.";
RL   Biochem. Biophys. Res. Commun. 250:558-564(1998).
CC   -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC       IMMUNE SYSTEM (BY SIMILARITY).
CC   -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC       MICROGLOBULIN) (BY SIMILARITY).
DR   EMBL; AF073485; AAC72900.1; -.
DR   EMBL; AF073484; AAC72900.1; JOINED.
DR   HSSP; Q30201; 1A6Z.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Glycoprotein; Transmembrane.
FT   NON_TER       1      1
SQ   SEQUENCE   334 AA;  38586 MW;  4C3E3A8248A39BA4 CRC64;

  Query Match           35.0%;  Score 530.5;  DB 7;  Length 334;
  Best Local Similarity   39.1%;  Pred. No. 2.5e-41;
  Matches  106;  Conservative   50;  Mismatches  112;  Indels    3;  Gaps    3;

Qy          4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWL 63
              |:||| |  :| |:   |:  | ::||||      ||  :|: ||| ||::  ::   |
Db         16 RTHSLRYFRLGVSDPIHGVPEFISVGYVDSHPITTYDSVTRQKEPRAPWMAENLAPDHWE 75

Qy         64 QLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDA 123
              : :| |:||  || |:   :  ::| |  ||| | ::|||: || || |: :| |||||
Db         76 RYTQLLRGWQQMFKVELKRLQRHYNHS-GSHTYQRMIGCELLEDGSTTGFLQYAYDGQDF 134

Qy        124 LEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQ 183
              | |  ||| | | :  |   |  || ::      : :|| :| | |:: || |:  | :
Db        135 LIFNKDTLSWLAVDNVAHTIKQAWEANQHELLYQKNWLEEECIAWLKRFLEYGKDTLQRT 194

Qy        184 VPPLVKVTHHVT-SSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTY 242
               ||||:|    |   || | |:|  :||  | | |:|: : :  :| :  |:||:|||||
Db        195 EPPLVRVNRKETFPGVTALFCKAHGFYPPEIYMTWMKNGEEI-VQEIDYGDILPSGDGTY 253

Qy        243 QGWITLAVPPGEEQRYTCQVEHPGLDQPLIV 273
              | | :: : |    |:| ||| |:   | |
Db        254 QAWASIELDPQSSNLYSCHVEHCGVHMVLQV 284


RESULT 10
Q9NPL2
ID   Q9NPL2      PRELIMINARY;      PRT;   341 AA.
AC   Q9NPL2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Mr1 protein.
GN   MR1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=20470599; PubMed=11019920;
RA   Parra-Cuadrado J.F., Navarro P. ., Mirones I., Setien F., Oteo M.,
RA   Martinez-Naves E.;
RT   "A study on the polymorphism of human MHC class I-related MR1 gene and
RT   identification of an MR1-like pseudogene.";
RL   Tissue Antigens 56:170-172(2000).
CC   -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC       IMMUNE SYSTEM (BY SIMILARITY).
CC   -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC       MICROGLOBULIN) (BY SIMILARITY).
DR   EMBL; AJ249778; CAB77667.1; -.
DR   PIR; A57136; A57136.
DR   HSSP; Q30201; 1A6Z.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Glycoprotein; Transmembrane.
SQ   SEQUENCE   341 AA;  39366 MW;  2990C1F3F0A1CAD9 CRC64;

  Query Match           35.0%;  Score 530.5;  DB 4;  Length 341;
  Best Local Similarity   39.1%;  Pred. No. 2.6e-41;
  Matches  106;  Conservative   50;  Mismatches  112;  Indels    3;  Gaps    3;

Qy          4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWL 63
              |:||| |  :| |:   |:  | ::||||      ||  :|: ||| ||::  ::   |
Db         23 RTHSLRYFRLGVSDPIHGVPEFISVGYVDSHPITTYDSVTRQKEPRAPWMAENLAPDHWE 82

Qy         64 QLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDA 123
              : :| |:||  || |:   :  ::| |  ||| | ::|||: || || |: :| |||||
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Db         83 RYTQLLRGWQQMFKVELKRLQRHYNHS-GSHTYQRMIGCELLEDGSTTGFLQYAYDGQDF 141

Qy        124 LEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQ 183

Db        142 LIFNKDTLSWLAVDNVAHTIKQAWEANQHELLYQKNWLEEECIAWLKRFLEYGKDTLQRT 201

Qy        184 VPPLVKVTHHVT-SSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTY 242

Db        202 EPPLVRVNRKETFPGVTALFCKAHGFYPPEIYMTWMKNGEEI-VQEIDYGDILPSGDGTY 260

Qy        243 QGWITLAVPPGEEQRYTCQVEHPGLDQPLIV 273

Db        261 QAWASIELDPQSSNLYSCHVEHCGVHMVLQV 291


RESULT 11
Q95460
ID   Q95460      PRELIMINARY;      PRT;   341 AA.
AC   Q95460;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Class I histocompatibility antigen-like protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymus;
RX   MEDLINE=95350662; PubMed=7624800;
RA   Hashimoto K., Hirai M., Kurosawa Y.;
RT   "A gene outside the human MHC related to classical HLA class I
RT   genes.";
RL   Science 269:693-695(1995).
CC   -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC       IMMUNE SYSTEM (BY SIMILARITY).
CC   -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC       MICROGLOBULIN) (BY SIMILARITY).
DR   EMBL; U22963; AAC50174.1; -.
DR   PIR; A57136; A57136.
DR   HSSP; Q30201; 1A6Z.
DR   Genew; HGNC:4975; MR1.
DR   GO; GO:0030106; F:MHC class I receptor activity; TAS.
DR   GO; GO:0006955; P:immune response; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Glycoprotein; Transmembrane.
SQ   SEQUENCE   341 AA;  39366 MW;  2990C1F3F0A1CAD9 CRC64;

  Query Match           35.0%;  Score 530.5;  DB 7;  Length 341;
  Best Local Similarity  39.1%;  Pred. No. 2.6e-41;
  Matches  106;  Conservative   50;  Mismatches  112;  Indels    3;  Gaps    3;

Qy          4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWL 63

Db         23 RTHSLRYFRLGVSDPIHGVPEFISVGYVDSHPITTYDSVTRQKEPRAPWMAENLAPDHWE 82

Qy         64 QLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDA 123

Db         83 RYTQLLRGWQQMFKVELKRLQRHYNHS-GSHTYQRMIGCELLEDGSTTGFLQYAYDGQDF 141

Qy        124 LEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQ 183

Db        142 LIFNKDTLSWLAVDNVAHTIKQAWEANQHELLYQKNWLEEECIAWLKRFLEYGKDTLQRT 201

Qy        184 VPPLVKVTHHVT-SSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTY 242

Db        202 EPPLVRVNRKETFPGVTALFCKAHGFYPPEIYMTWMKNGEEI-VQEIDYGDILPSGDGTY 260

Qy        243 QGWITLAVPPGEEQRYTCQVEHPGLDQPLIV 273

Db        261 QAWASIELDPQSSNLYSCHVEHCGVHMVLQV 291


RESULT 12
Q9BCU3
ID   Q9BCU3      PRELIMINARY;      PRT;   341 AA.
AC   Q9BCU3;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   MHC class I related protein, MR1B1 isoform.
GN   MR1.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Martinez-Naves E.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Parra-Cuadrado J.F., Garcia-Pavia P., Gomez del Moral M.;
RT   "Identification of MR1 cDNA sequences in non-human primates.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC       IMMUNE SYSTEM (BY SIMILARITY).
CC   -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC       MICROGLOBULIN) (BY SIMILARITY).
DR   EMBL; AJ275984; CAC34272.1; -.
DR   HSSP; Q30201; 1A6Z.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Glycoprotein; Transmembrane.
FT   VARIANT     197    197       I -> T (IN REF. 2).
SQ   SEQUENCE   341 AA;  39394 MW;  FBFA822BCAB2C7A8 CRC64;

  Query Match           35.0%;  Score 530.5;  DB 7;  Length 341;
  Best Local Similarity  39.1%;  Pred. No. 2.6e-41;
  Matches  106;  Conservative   51;  Mismatches  111;  Indels    3;  Gaps    3;

Qy          4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWL 63

Db         23 RTHSLRYFRLGVSDPIHGVPEFISVGYVDSHPITTYDSVTRQKEPRAPWMAENLAPDHWE 82

Qy         64 QLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDA 123

Db         83 RYTQLLRGWQQMFKVELKRLQRHYNHS-GSHTYQRMIGCELLEDGSTTGFLQYAYDGQDF 141

Qy        124 LEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQ 183

Db        142 LIFNKDTLSWLAVDNVAHTIKQAWEANQHELLYQKNWLEEECIAWLKRFLEYGKDILQRT 201

Qy        184 VPPLVKVTHHVT-SSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTY 242

Db        202 EPPLVRVNRKETFPGVTALFCKAHGFYPPEIYMTWMKNGEEI-VQEIDYGDILPSGDGTY 260

Qy        243 QGWITLAVPPGEEQRYTCQVEHPGLDQPLIV 273

Db        261 QAWASIELDPQSSNLYSCHVEHCGVHMVLQV 291
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Qy        243 QGWITLAVPPGEEQRYTCQVEHPGLDQPLIV 273
              | | :: : |     |:| ||| |:   | |
Db        261 QTWASVELDPQSSNLYSCHVEHCGVHMVLQV 291


RESULT 13
Q9BCU4
ID   Q9BCU4      PRELIMINARY;      PRT;   341 AA.
AC   Q9BCU4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   MHC class I related protein, MR1B1 isoform.
GN   MR1.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Martinez-Naves E.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Parra-Cuadrado J.F., Garcia-Pavia P., Gomez del Moral M.;
RT   "Identification of MR1 cDNA sequences in non-human primates.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC       IMMUNE SYSTEM (BY SIMILARITY).
CC   -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC       MICROGLOBULIN) (BY SIMILARITY).
DR   EMBL; AJ275982; CAC34274.1; -.
DR   HSSP; Q30201; 1A6Z.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Glycoprotein; Transmembrane.
FT   VARIANT     197    197       T -> I (IN REF. 2).
SQ   SEQUENCE   341 AA;  39382 MW;  DFF16AF1FAB2D272 CRC64;

  Query Match             34.8%;  Score 527.5;  DB 7;  Length 341;
  Best Local Similarity   39.1%;  Pred. No. 4.9e-41;
  Matches  106;  Conservative   50;  Mismatches  112;  Indels    3;  Gaps    3;

Qy          4 RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWL 63
              |:||| |  :| |:   |:  | ::|||| |  :|: ||| ||::  ::   |
Db         23 RTHSLRYFRLGVSDPIHGVPEFISVGYVDSHPITTYDSVTRQKEPRAPWMAENLAPDHWE 82

Qy         64 QLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDA 123
              : :| |:||  || |:   :  ::| |  ||| | ::|||: || || |: :| |||||
Db         83 RYTQLLRGWQQMFKVELKRLQRHYNHS-GSHTYQRMIGCELLEDGSTTGFLQYAYDGQDF 141

Qy        124 LEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQ 183
              | |  ||| | | :  |   | || ::     : :|| :| | |:: || |:  | :
Db        142 LIFNKDTLSWLAVDNVAHTIKQAWEANQHELLYQKNWLEEECIAWLKRFLEYGKDTLQRT 201

Qy        184 VPPLVKVTHHVT-SSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTY 242
               ||||:|    |   || | |:|  :||  | | |:|: : :  :| :  |:||:|||||
Db        202 EPPLVRVNRKETFPGVTALFCKAHGFYPPEIYMTWMKNGEEI-VQEIDYGDILPSGDGTY 260

Qy        243 QGWITLAVPPGEEQRYTCQVEHPGLDQPLIV 273
              | | :: : |     |:| ||| |:   | |
Db        261 QTWASVELDPQSSNLYSCHVEHCGVHMVLQV 291


RESULT 14
Q8HX66
ID   Q8HX66      PRELIMINARY;      PRT;   356 AA.
AC   Q8HX66;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   MHC class I antigen (Fragment).
GN   SLA-1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Martens G.W., Baker J.E., Smith D.M.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY135589; AAN35107.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   356 AA;  39585 MW;  94FC7A461DBF555B CRC64;

  Query Match             34.0%;  Score 515;  DB 7;  Length 356;
  Best Local Similarity   39.9%;  Pred. No. 7.6e-40;
  Matches  110;  Conservative   47;  Mismatches  111;  Indels    8;  Gaps    7;

Qy          6 HSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMWL 63
              ||| | :   |  ||| | | |:||||  || :| :  : |:||| ||:      : |
Db         19 HSLRYFYTAVSRPDLGDSRFIAVGYVDDTQFVRFDSDAPNPRMEPRAPWIQQE-GQEYWD 77

Qy         64 QLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDN-STEGYWKYGYDGQ 121
              : :::  |      ||  |:   :| |:  |||:| : ||::  |     || :  |||
Db         78 EETRNAMGSAQNDRVDLKTLRGYYNQSEAGSHTIQRMYGCDVGPDGLLLRGYDQDAYDGA 137

Qy        122 DALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLD 181
              | :   |  | ||:  |  || :||   : | | |:|||  |   ||: ||:|:  |
Db        138 DYIALNEDLRSWTAADTAAQITKRKWEAANV-AEQERSYLEGTCVEWLQKYLEMGKDTLQ 196

Qy        182 QQVPPLVKVTHHVTSSV-TTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              :  ||   || | :| :  |||| || :||: |:: | :: |   ::: |  :  |:|||
Db        197 RAEPPKTHVTRHPSSDLGVTLRCWALGFYPKEISLTWQREGQD-QSQDMELVETRPSGDG 255

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |:| |  | |||||| ||| |:| || : :|| : |:
Db        256 TFQKWAALVVPPGEEQSYTCHVQHEGLQEPLTLRWD 291


RESULT 15
Q30990
ID   Q30990      PRELIMINARY;      PRT;   332 AA.
AC   Q30990;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Chimpanzee MHC class I ChlA chain (Fragment).
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89235215; PubMed=2715640;
RA   Parham P., Lawlor D.A., Lomen C.E., Ennis P.D.;
RT   "Diversity and diversification of HLA-A,B,C alleles.";
RL   J. Immunol. 142:3937-3950(1989).
CC   -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC       IMMUNE SYSTEM (BY SIMILARITY).
CC   -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC       MICROGLOBULIN) (BY SIMILARITY).
DR   EMBL; M24047; AAA35426.1; -.
DR   PIR; S06424; S06424.
DR   HSSP; Q95352; 1HHK.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Glycoprotein; Transmembrane.
FT   NON_TER     332    332
SQ   SEQUENCE   332 AA;  37433 MW;  9AA9A55DF9E79360 CRC64;

  Query Match             33.9%;  Score 514;  DB 7;  Length 332;
  Best Local Similarity   40.1%;  Pred. No. 8.7e-40;
  Matches  111;  Conservative   43;  Mismatches  115;  Indels    8;  Gaps    7;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |    |   | |:||||  || :| :  |:|:||| ||:      : |
Db         26 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
               | ::| |      ||  |:   :| |:: |||:|:: ||::  |     || :  |||
Db         85 DQETRSAKAHSQTDRVDLGTLRGYYNQSEDGSHTIQIMYGCDVGSDGRFLRGYRQDAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| :    |   | ||:  |  || :||     | | |||||  |   |:: || |:  |
Db        145 KDYIALNEDLRSWTAADMAAQITKRKWEAAH-AAEQQRAYLEGTCVEWLRRYLENGKETL 203

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
               :  ||   :||| ::    |||| || :||  ||: | :| :    :: |  :  | ||
Db        204 QRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGED-QTQDTELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || ||||||||  |:| || :|| : ||
Db        263 GTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE 299


Search completed: May  4, 2004, 11:38:33
Job time : 35.6667 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 4, 2004, 11:32:18 ; Search time 49.3333 Seconds
(without alignments)
1580.739 Million cell updates/sec

Title: US-10-092-404-3
Perfect score: 1514
Sequence: 1 RLLRSHSLHYLFMGASEQDL.....RYTCQVEHPGLDQPLIVIWE 276

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1514	100.0	276	2	AAW94297	Aaw94297 HFE mutan
2	1514	100.0	276	6	ABG72687	Abg72687 Human hae
3	1502	99.2	276	2	AAW94295	Aaw94295 Wild-type
4	1502	99.2	276	6	ABG72685	Abg72685 Human hae
5	1502	99.2	348	2	AAW36499	Aaw36499 Hereditar
6	1502	99.2	348	3	AAB19149	Aab19149 A human h
7	1502	99.2	348	4	AAB36869	Aab36869 Human her
8	1497	98.9	438	5	AAU80035	Aau80035 Beta 2 mi
9	1495	98.7	276	6	ABU62091	Abu62091 HFE polyp
10	1493	98.6	276	2	AAW94296	Aaw94296 HFE mutan
11	1493	98.6	276	6	ABG72686	Abg72686 Human hae
12	1493	98.6	276	6	ABU62093	Abu62093 HFE mutan
13	1493	98.6	348	4	AAB36871	Aab36871 Human her
14	1491	98.5	348	4	AAB36870	Aab36870 Human her
15	1486	98.2	276	6	ABU62092	Abu62092 HFE mutan
16	1482	97.9	348	4	AAB36872	Aab36872 Human her
17	517	34.1	361	4	AAB36873	Aab36873 Rabbit le
18	508	33.6	365	4	AAB36874	Aab36874 MHC class
19	504	33.3	92	6	ABP68379	Abp68379 Human col
20	500	33.0	274	3	AAY68275	Aay68275 Human leu
21	500	33.0	274	3	AAY52929	Aay52929 HLA-A2/A2
22	500	33.0	274	4	AAB58690	Aab58690 HLA-A2/A2
23	500	33.0	280	4	AAU10225	Aau10225 Human leu
24	500	33.0	280	6	ABU08672	Abu08672 Human his
25	500	33.0	415	4	AAU10224	Aau10224 Human par
26	500	33.0	415	6	ABU08671	Abu08671 Human sin
27	500	33.0	510	6	AAE36053	Aae36053 B2M-aTacV
28	499	33.0	365	3	AAY68265	Aay68265 Human leu
29	499	33.0	365	3	AAY52919	Aay52919 HLA-A2/A2
30	499	33.0	365	4	AAB58680	Aab58680 HLA-A2/A2
31	499	33.0	368	4	AAM24017	Aam24017 Human EST
32	498	32.9	274	3	AAY68276	Aay68276 Human leu
33	498	32.9	274	3	AAY52930	Aay52930 HLA-A2/A2
34	498	32.9	274	4	AAB58691	Aab58691 HLA-A2/A2
35	498	32.9	365	3	AAY68268	Aay68268 Human leu
36	498	32.9	365	3	AAY52922	Aay52922 HLA-A2/A2
37	498	32.9	365	4	AAB58683	Aab58683 HLA-A2/A2
38	497	32.8	274	1	AAP80911	Aap80911 Consensus
39	497	32.8	365	3	AAY68267	Aay68267 Human leu
40	497	32.8	365	3	AAY52921	Aay52921 HLA-A2/A2
41	497	32.8	365	4	AAB58682	Aab58682 HLA-A2/A2
42	496	32.8	274	3	AAY68274	Aay68274 Human leu
43	496	32.8	274	3	AAY52928	Aay52928 HLA-A2/A2
44	496	32.8	274	4	AAB58689	Aab58689 HLA-A2/A2
45	496	32.8	365	3	AAY68266	Aay68266 Human leu

ALIGNMENTS

RESULT 1
AAW94297
ID AAW94297 standard; peptide; 276 AA.
XX
AC AAW94297;
XX
DT 27-APR-1999 (first entry)
XX
DE HFE mutant (H111A/H145A-HFE) polypeptide sequence.
XX
KW HFE; beta-2-microglobulin; beta2m; iron overload; hemochromatosis;
KW transfusion; protein replacement therapy; hereditary hemochromatosis;
KW transferrin receptor; iron deficiency; anemia; mutant.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 2
FT /note= "indicated in the sequence listing as Arg"
FT Misc-difference 89
FT /label= H111A
FT /note= "wild type His (of the mature protein sequence) is
FT replaced by Ala"
FT Misc-difference 123
FT /label= H145A
FT /note= "wild type His (of the mature protein sequence) is
FT replaced by Ala"
XX
PN WO9856814-A1.
XX
PD 17-DEC-1998.
XX
PF 12-JUN-1998; 98WO-US012436.
XX
PR 13-JUN-1997; 97US-00876010.
XX
PA (PROG-) PROGENITOR INC.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Feder JN, Bjorkman PJ, Schatzman RC;
XX
DR WPI; 1999-080886/07.
XX
PT New treatment of an iron overload disease - comprises use of HFE
PT polypeptides provided in a complex with full length, wild type human
PT (2m), useful in protein replacement therapy.
XX
PS Claim 5; Page 15; 36pp; English.

XX
CC The present sequence represents a H111A/H145A-HFE mutant polypeptide. The
CC HFE polypeptides (AAW94295-297) provided in a complex with full length,
CC wild type human beta-2-microglobulin (beta2m) form compositions in the
CC treatment of primary iron overload diseases (e.g. hemochromatosis), or
CC other iron overload conditions resulting from secondary causes (e.g.
CC repeated transfusions). Data regarding the structure and function
CC correlations of HFE polypeptides is useful in designing drugs that
CC modulate the HFE gene and HFE activity. The polypeptides are also useful
CC in protein replacement therapy for individuals possessing a defective HFE
CC gene (e.g. Hereditary hemochromatosis). (Ant)agonists of the polypeptides
CC are also useful in treating primary and secondary iron overload diseases.
CC The modulators of the transferrin receptor are useful in treating iron
CC deficiency conditions such as anemia, and in modulating the amount of
CC iron transported into a cell. The HFE polypeptides provide a molecular
CC basis for the relationship between HFE and iron metabolism, which enables
CC treatment of iron overload and deficiency diseases
XX
SQ Sequence 276 AA;

Query Match 100.0%; Score 1514; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 3.9e-131;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
Db 1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60

Qy 61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
Db 61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

Qy 121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
Db 121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

Qy 181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
Db 181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240

Qy 241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
Db 241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276

RESULT 2
ABG72687
ID ABG72687 standard; protein; 276 AA.
XX
AC ABG72687;
XX
DT 05-MAR-2003 (first entry)
XX
DE Human haemochromatosis (HFE) mature protein, mutant H89A/H123A.
XX
KW Human; haemochromatosis; HFE; hereditary haemochromatosis;
KW iron overload disease; iron deficiency disease; Beta2-microglobulin;
KW Beta2m; transferrin receptor; anaemia; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 89
FT /note= "Wild-type His substituted by Ala"
FT Misc-difference 123
FT /note= "Wild-type His substituted by Ala"
XX
PN US6391852-B1.
XX
PD 21-MAY-2002.
XX
PF 12-JUN-1998; 98US-00094964.
XX
PR 13-JUN-1997; 97US-00876010.
XX
PA (BIRA) BIO-RAD LAB INC.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Feder JN, Bjorkman PJ, Schatzman RC;
XX
DR WPI; 2003-155377/15.
XX
PT Method of treating an iron overload disease comprises administration of a
PT soluble complex comprising a 276 amino acid HFE polypeptide and a full
PT length, wild-type human beta2m.
XX
PS Claim 3; Col 2; 17pp; English.
XX
CC The invention relates to a method of treating an iron overload disease
CC comprising administration of a soluble complex comprising a 276 amino
CC acid mature HFE (hereditary haemochromatosis gene protein) polypeptide
CC (ABG72685-ABG72687) and a full length, wild-type human beta2m (beta2-
CC microglobulin). In a HeLa cell based assay, binding and uptake of ^1^2^5I
CC -transferrin in the presence of purified H63D-HFE/beta2m heterodimers was
CC determined. At a concentration of 250 nM H63D-HFE/ beta2m heterodimers,
CC the transferrin receptor (TfR) displayed a KD for transferrin of 28 nM.
CC At the same concentration of normal HFE/beta_2m heterodimers, TfR
CC displayed a KD for transferrin of 40 nM. In the absence of any
CC HFE/beta_2m heterodimers, TfR displayed a KD for transferrin of 7nM. It
CC was observed that H63D-HFE/beta_2m heterodimers were 30-40 % less
CC efficient in decreasing TfR affinity for transferrin compared to wild-
CC type HFE. The method is useful for treating iron overload diseases and
CC iron deficiency e.g. anaemia. The present sequence is the H111A/H145A
CC (residues 111 and 145 of the full length protein, 89/123 of the mature
CC form) mutant from of mature HFE used to investigate the role of the His
CC residues in transferrin receptor binding to transferrin
XX
SQ Sequence 276 AA;

Query Match 100.0%; Score 1514; DB 6; Length 276;
Best Local Similarity 100.0%; Pred. No. 3.9e-131;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
Db 1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60

Qy 61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
Db 61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

Qy 121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
Db 121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

Qy 181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
Db 181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240

Qy 241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
Db 241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276

RESULT 3
AAW94295
ID AAW94295 standard; peptide; 276 AA.
XX
AC AAW94295;
XX
DT 27-APR-1999 (first entry)
XX
DE Wild-type HFE polypeptide sequence.
XX
KW HFE; beta-2-microglobulin; beta2m; iron overload; hemochromatosis;

KW transfusion; protein replacement therapy; hereditary hemochromatosis;
KW transferrin receptor; iron deficiency; anemia.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 2
FT /note= "indicated in the sequence listing as Arg"
XX
PN WO9856814-A1.
XX
PD 17-DEC-1998.
XX
PF 12-JUN-1998; 98WO-US012436.
XX
PR 13-JUN-1997; 97US-00876010.
XX
PA (PROG-) PROGENITOR INC.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Feder JN, Bjorkman PJ, Schatzman RC;
XX
DR WPI; 1999-080886/07.
XX
PT New treatment of an iron overload disease - comprises use of HFE
PT polypeptides provided in a complex with full length, wild type human
PT (2m), useful in protein replacement therapy.
XX
PS Claim 1; Page 13; 36pp; English.
XX
CC The present sequence represents a wild-type HFE polypeptide. The HFE
CC polypeptides (AAW94295-297) provided in a complex with full length, wild
CC type human beta-2-microglobulin (beta2m) form compositions in the
CC treatment of primary iron overload diseases (e.g. hemochromatosis), or
CC other iron overload conditions resulting from secondary causes (e.g.
CC repeated transfusions). Data regarding the structure and function
CC correlations of HFE polypeptides is useful in designing drugs that
CC modulate the HFE gene and HFE activity. The polypeptides are also useful
CC in protein replacement therapy for individuals possessing a defective HFE
CC gene (e.g. Hereditary hemochromatosis). (Ant)agonists of the polypeptides
CC are also useful in treating primary and secondary iron overload diseases.
CC The modulators of the transferrin receptor are useful in treating iron
CC deficiency conditions such as anemia, and in modulating the amount of
CC iron transported into a cell. The HFE polypeptides provide a molecular
CC basis for the relationship between HFE and iron metabolism, which enables
CC treatment of iron overload and deficiency diseases
XX
SQ Sequence 276 AA;

Query Match 99.2%; Score 1502; DB 2; Length 276;
Best Local Similarity 99.3%; Pred. No. 5e-130;
Matches 274; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
```

RESULT 4
ABG72685
ID ABG72685 standard; protein; 276 AA.
XX
AC ABG72685;
XX
DT 05-MAR-2003 (first entry)
XX
DE Human haemochromatosis (HFE) mature protein.
XX
KW Human; haemochromatosis; HFE; hereditary haemochromatosis;
KW iron overload disease; iron deficiency disease; Beta2-microglobulin;
KW Beta2m; transferrin receptor; anaemia.
XX
OS Homo sapiens.
XX
PN US6391852-B1.
XX
PD 21-MAY-2002.
XX
PF 12-JUN-1998; 98US-00094964.
XX
PR 13-JUN-1997; 97US-00876010.
XX
PA (BIRA) BIO-RAD LAB INC.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Feder JN, Bjorkman PJ, Schatzman RC;
XX
DR WPI; 2003-155377/15.
XX
PT Method of treating an iron overload disease comprises administration of a
PT soluble complex comprising a 276 amino acid HFE polypeptide and a full
PT length, wild-type human beta2m.
XX
PS Claim 1; Col 1; 17pp; English.
XX
CC The invention relates to a method of treating an iron overload disease
CC comprising administration of a soluble complex comprising a 276 amino
CC acid mature HFE (hereditary haemochromatosis gene protein) polypeptide
CC (ABG72685-ABG72687) and a full length, wild-type human beta2m (beta2-
CC microglobulin). In a HeLa cell based assay, binding and uptake of ^1^2^5I
CC -transferrin in the presence of purified H63D-HFE/beta2m heterodimers was
CC determined. At a concentration of 250 nM H63D-HFE/ beta2m heterodimers,
CC the transferrin receptor (TfR) displayed a KD for transferrin of 28 nM.
CC At the same concentration of normal HFE/beta_2m heterodimers, TfR
CC displayed a KD for transferrin of 40 nM. In the absence of any
CC HFE/beta_2m heterodimers, TfR displayed a KD for transferrin of 7nM. It
CC was observed that H63D-HFE/beta_2m heterodimers were 30-40 % less
CC efficient in decreasing TfR affinity for transferrin compared to wild-
CC type HFE. The method is useful for treating iron overload diseases and
CC iron deficiency e.g. anaemia. The present sequence is wild-type mature
CC HFE
XX
SQ Sequence 276 AA;

Query Match 99.2%; Score 1502; DB 6; Length 276;
Best Local Similarity 99.3%; Pred. No. 5e-130;
Matches 274; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
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Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276


RESULT 5
AAW36499
ID   AAW36499 standard; protein; 348 AA.
XX
AC   AAW36499;
XX
DT   14-APR-1998  (first entry)
XX
DE   Hereditary haemochromatosis gene product.
XX
KW   Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy;
KW   prenatal screening; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 63
FT                   /note= "substituted by Asp in 24s2 mutant"
FT   Misc-difference 65
FT                   /note= "substituted by Cys in 24d7 variant"
FT   Misc-difference 282
FT                   /note= "substituted by Tyr in 24d1 mutant"
XX
PN   WO9738137-A1.
XX
PD   16-OCT-1997.
XX
PF   04-APR-1997;   97WO-US006254.
XX
PR   04-APR-1996;   96US-00630912.
PR   16-APR-1996;   96US-00632673.
PR   23-MAY-1996;   96US-00652265.
XX
PA   (MERC-) MERCATOR GENETICS INC.
XX
PI   Thomas WJ,  Drayna DT,  Feder JN,  Gnirke A,  Ruddy D,  Tsuchihashi Z;
PI   Wolff RK;
XX
DR   WPI; 1997-512743/47.
DR   N-PSDB; AAT96690, AAT96691.
XX
PT   Hereditary haemochromatosis gene and variants - useful for diagnosis and
PT   treatment of hereditary haemochromatosis disease.
XX
PS   Disclosure; Fig 4; 115pp; English.
XX
CC   This polypeptide is the expression product of a novel human gene (see
CC   AAT96690) whose mutated form is associated with hereditary
CC   haemochromatosis (HH). A single mutation (24d1) in the HH gene appears
CC   responsible for the majority of HH disease. This comprises a G to A
CC   substitution that is present in 86% of affected chromosomes and in 4% of
CC   unaffected chromosomes. It results in a Cys to Tyr substitution in the
CC   encoded protein at a critical disulphide bridge important for secondary
CC   structure. The following are claimed: the 10825 bp genomic DNA sequence
CC   (I), a 1437 bp cDNA sequence (Ia) (see AAT96691) and their 24d1, 24d2 and
CC   24d7 variants; a cloning or expression vector; host cells; a peptide
CC   product chosen from the HH gene product, its variants (24d1, 24d2 and
CC   24d7), or a peptide of at least 56 amino acid residues of these; an
CC   antibody produced using the peptide as an immunogen; a method to
CC   determine the presence or absence of the common HH gene mutation; an
CC   animal model for the HH disease; metal chelation agents, T-cell
CC   differentiation factors and therapeutic agents for the mitigation of
CC   injury due to oxidative process in vivo or mitigation of iron overload; a
CC   method for screening potential therapeutic agents for activity in
CC   connection with HH disease; an antisense oligonucleotide directed against
CC   a transcriptional product of a nucleic acid sequence as above; and
CC   oligonucleotides or pairs of oligonucleotides covering a range of
CC   nucleotides from (I), (Ia) or their variants, useful for detecting a
CC   polymorphism in the HH gene. The invention also relates to methods for
CC   screening for HH homozygotes, to HH diagnosis, prenatal screening and
CC   diagnosis, and therapies of HH disease, including gene therapy, protein-
CC   and antibody-based therapeutics, and small molecule therapeutics
XX
SQ   Sequence 348 AA;

  Query Match             99.2%;  Score 1502;  DB 2;  Length 348;
  Best Local Similarity   99.3%;  Pred. No. 6.7e-130;
  Matches  274;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 6
AAB19149
ID   AAB19149 standard; protein; 348 AA.
XX
AC   AAB19149;
XX
DT   19-FEB-2001  (first entry)
XX
DE   A human histocompatibility iron loading (HFE) protein.
XX
KW   Human; histocompatibility iron loading protein; HFE protein;
KW   major histocompatibility complex; non-classical class I gene;
KW   chromosome 6p; iron disorder; haemochromatosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /note= "signal peptide"
FT   Misc-difference 63
FT                   /note= "when nucleotide 187 is mutated to G, then this
FT                   residue is Asp"
FT   Misc-difference 65
FT                   /note= "when nucleotide 193 is mutated to T, then this
FT                   residue is Cys"
FT   Domain          80. .108
FT                   /note= "alpha1 domain"
FT   Misc-difference 93
FT                   /note= "when nucleotide 277 is mutated to C, then this
FT                   residue is Arg"
FT   Misc-difference 105
FT                   /note= "when nucleotide 314 is mutated to C, then this
FT                   residue is Thr"
XX
PN   WO200058515-A1.
XX
PD   05-OCT-2000.
```

XX
PF 24-MAR-2000; 2000WO-US007982.
XX
PR 26-MAR-1999; 99US-00277457.
XX
PA (BILL-) BILLUPS-ROTHENBERG INC.
XX
PI Rothenberg BE, Sawada-Hirai R, Barton JC;
XX
DR WPI; 2000-647244/62.
DR N-PSDB; AAA96769.
XX
PT Diagnosing an iron disorder e.g. hemochromatosis or a genetic
PT susceptibility to develop it, by determining the presence of a mutation
PT in exon 2 or an intron of a histocompatibility iron loading nucleic acid.
XX
PS Disclosure; Page 3; 55pp; English.
XX
CC The present sequence represents a human histocompatibility iron loading
CC (HFE) protein. The HFE gene is a major histocompatibility (MHC) non-
CC classical class I gene located on chromosome 6p. Mutations in the gene
CC lead to iron disorders. The specification describes a method for
CC diagnosing an iron disorder or a genetic susceptibility to develop the
CC disorder in a mammal. The method comprises determining the presence of a
CC mutation in exon 2 or an intron of a HFE gene or protein. The mutation is
CC not a C to G missense mutation at nucleotide 187 of the sequence given in
CC A96769 (Genbank Accession number U60319). The presence of the mutation
CC indicates the disorder or the genetic susceptibility to the disorder. The
CC method is used to diagnose an iron disorder e.g. haemochromatosis, or a
CC genetic susceptibility to develop it
XX
SQ Sequence 348 AA;

Query Match 99.2%; Score 1502; DB 3; Length 348;
Best Local Similarity 99.3%; Pred. No. 6.7e-130;
Matches 274; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298
```

RESULT 7
AAB36869
ID AAB36869 standard; protein; 348 AA.
XX
AC AAB36869;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human hereditary hemochromatosis protein.
XX
KW HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload.
XX
OS Homo sapiens.
XX

PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-00834497.
XX
PR 04-APR-1996; 96US-00630912.
PR 16-APR-1996; 96US-00632673.
PR 23-MAY-1996; 96US-00652265.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI; 2001-006341/01.
DR N-PSDB; AAC68425.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful for
PT treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload.
XX
PS Claim 1; Fig 4; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene
XX
SQ Sequence 348 AA;

Query Match 99.2%; Score 1502; DB 4; Length 348;
Best Local Similarity 99.3%; Pred. No. 6.7e-130;
Matches 274; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298
```

RESULT 8
AAU80035
ID AAU80035 standard; protein; 438 AA.
XX
AC AAU80035;
XX
DT 15-JUL-2002 (first entry)
XX
DE Beta 2 microglobulin (beta2M)/HFE monochain.
XX
KW Human; beta 2 microglobulin; beta2M/HFE monochain; HFE; ischaemia;
KW iron absorption regulator; intracellular iron absorption; lung injury;
KW haemochromatosis; transfusion; thalassaemia; haemolytic anaemia;
KW chronic infection; transferrin receptor; TfR; brain tumour; cancer;
KW oxidative stress disorder; tissue damage; vascular disease; inflammation;

KW atherosclerosis; autoimmune disease; inflammatory condition.
XX
OS Homo sapiens.
XX
PN WO200224929-A2.
XX
PD 28-MAR-2002.
XX
PF 24-SEP-2001; 2001WO-US029873.
XX
PR 22-SEP-2000; 2000US-0234843P.
XX
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA (MCIN/) MCINNIS P.
XX
PI Ehrlich R, Rotem-Yehudar R, Laham N;
XX
DR WPI; 2002-383192/41.
DR N-PSDB; ABK49917.
XX
PT Soluble beta 2 microglobulin/HFE monochain useful for treating iron-
PT overload conditions e.g. thalassemia and chronic infections, comprises
PT human beta 2 microglobulin linked to alpha domains of HFE by a linker
PT peptide.
XX
PS Example 2; Fig 2; 77pp; English.
XX
CC The invention relates to a soluble polypeptide (I) of beta 2
CC microglobulin (beta2m)/HFE monochain comprising human beta2m (or its
CC analogue or active fragment), linked to alpha1-alpha3 domains of human
CC HFE (a central regulator of iron absorption; undefined), or its analogue
CC or active fragment, by a flexible linker peptide, or a functional
CC derivative or salt of (I). (I) is useful for reducing intracellular iron
CC absorption in patients having hereditary haemochromatosis, transfusions,
CC thalassaemias, haemolytic anaemia or chronic infections, and for
CC delivering a therapeutic to cells that over-express transferrin receptor
CC (TfR) which are preferably lymphocytes or leukocytes, across the blood-
CC brain barrier. (I) is further useful for treating brain tumour. (I) is
CC also useful for treating oxidative stress disorders resulting in tissue
CC damage e.g. vascular diseases, inflammation, atherosclerosis, lung
CC injury, ischaemia, etc. A DNA molecule (II) encoding (I) is useful as a
CC platform for drug delivery of therapeutic use for cancer, autoimmune
CC diseases and inflammatory conditions. The monochain manifests specific
CC characteristics advantageous for drug delivery systems. It is a soluble,
CC stable and fully conformed protein. It binds specifically to transferrin
CC receptor (TfR) and therefore targets cells that over-express this
CC receptor. It is continuously internalised by the target cells, thus
CC enabling efficient drug delivery. It dissociates from the receptor in the
CC cells, minimising side effects. It negatively regulates iron absorption,
CC reducing growth of undesired cells and preventing lymphocyte activation.
CC It is not diluted in the blood as is transferrin. It should not induce an
CC immune response since it is a self non-polymeric protein and delivery of
CC drugs via monochain is expected to overcome drug-resistance since it is a
CC natural TfR-binding protein. The present sequence represents the amino
CC acid sequence of beta2m/HFE monochain
XX
SQ Sequence 438 AA;

Query Match 98.9%; Score 1497; DB 5; Length 438;
Best Local Similarity 99.3%; Pred. No. 2.6e-129;
Matches 273; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
Db 135 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 194

Qy 61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
Db 195 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 254

Qy 121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
Db 255 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 314

Qy 181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
Db 315 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 374

Qy 241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIW 275
Db 375 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIW 409

RESULT 9
ABU62091
ID ABU62091 standard; protein; 276 AA.
XX
AC ABU62091;
XX
DT 01-OCT-2003 (first entry)
XX
DE HFE polypeptide useful for treating iron diseases.
XX
KW Iron overload disease; iron deficiency disease; HFE polypeptide;
KW beta2 microglobulin; beta2m; hereditary haemochromatosis; HH; anaemia;
KW protein replacement therapy; defective HFE gene; human; antianaemic;
KW mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2003073627-A1.
XX
PD 17-APR-2003.
XX
PF 04-MAR-2002; 2002US-00092404.
XX
PR 13-JUN-1997; 97US-00876010.
PR 12-JUN-1998; 98US-00094964.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Feder JN, Bjorkman PJ, Schatzman RC;
XX
DR WPI; 2003-567313/53.
XX
PT Treating an iron overload disease (e.g. hemochromatosis) or an iron
PT deficiency disease (e.g. anemia), comprises administering to a patient an
PT HFE polypeptide and full-length, wild type human beta-2 microglobulin.
XX
PS Claim 1; Page 1; 14pp; English.
XX
CC The present invention relates to a method for treating iron overload
CC diseases and iron deficiency diseases. The method comprises administering
CC to a patient an HFE polypeptide. The HFE polypeptide is provided in a
CC complex with full-length, wild type human beta2 microglobulin (beta2m).
CC The method and HFE polypeptide are useful for diagnosing or treating an
CC iron overload disease (e.g. hereditary haemochromatosis, HH) or an iron
CC deficiency disease (e.g. anaemia). The HFE polypeptide is also useful in
CC protein replacement therapy for individuals having a defective HFE gene.
CC The present sequence represents an HFE polypeptide useful for treating
CC iron diseases
XX
SQ Sequence 276 AA;

Query Match 98.7%; Score 1495; DB 6; Length 276;
Best Local Similarity 98.9%; Pred. No. 2.2e-129;
Matches 273; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
Db 1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60

Qy 61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
Db 61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

```
Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        181 DQQVPPLVKVTHHVTSSVTTLRCPALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
```

RESULT 10
AAW94296
ID AAW94296 standard; peptide; 276 AA.
XX
AC AAW94296;
XX
DT 27-APR-1999 (first entry)
XX
DE HFE mutant (H63D-HFE) polypeptide sequence.
XX
KW HFE; beta-2-microglobulin; beta2m; iron overload; hemochromatosis;
KW transfusion; protein replacement therapy; hereditary hemochromatosis;
KW transferrin receptor; iron deficiency; anemia; mutant.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 2
FT /note= "indicated in the sequence listing as Arg"
FT Misc-difference 41
FT /label= H63D
FT /note= "wild type His (of the mature protein sequence) is
FT replaced by Asp"
XX
PN WO9856814-A1.
XX
PD 17-DEC-1998.
XX
PF 12-JUN-1998; 98WO-US012436.
XX
PR 13-JUN-1997; 97US-00876010.
XX
PA (PROG-) PROGENITOR INC.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Feder JN, Bjorkman PJ, Schatzman RC;
XX
DR WPI; 1999-080886/07.
XX
PT New treatment of an iron overload disease - comprises use of HFE
PT polypeptides provided in a complex with full length, wild type human
PT (2m), useful in protein replacement therapy.
XX
PS Claim 3; Page 14; 36pp; English.
XX
CC The present sequence represents a H63D-HFE mutant polypeptide. The HFE
CC polypeptides (AAW94295-297) provided in a complex with full length, wild
CC type human beta-2-microglobulin (beta2m) form compositions in the
CC treatment of primary iron overload diseases (e.g. hemochromatosis), or
CC other iron overload conditions resulting from secondary causes (e.g.
CC repeated transfusions). Data regarding the structure and function
CC correlations of HFE polypeptides is useful in designing drugs that
CC modulate the HFE gene and HFE activity. The polypeptides are also useful
CC in protein replacement therapy for individuals possessing a defective HFE
CC gene (e.g. Hereditary hemochromatosis). (Ant)agonists of the polypeptides
CC are also useful in treating primary and secondary iron overload diseases.
CC The modulators of the transferrin receptor are useful in treating iron
CC deficiency conditions such as anemia, and in modulating the amount of
CC iron transported into a cell. The HFE polypeptides provide a molecular
CC basis for the relationship between HFE and iron metabolism, which enables
CC treatment of iron overload and deficiency diseases
XX
SQ Sequence 276 AA;

```
  Query Match             98.6%;  Score 1493;  DB 2;  Length 276;
  Best Local Similarity   98.9%;  Pred. No. 3.4e-129;
  Matches  273;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
```

RESULT 11
ABG72686
ID ABG72686 standard; protein; 276 AA.
XX
AC ABG72686;
XX
DT 05-MAR-2003 (first entry)
XX
DE Human haemochromatosis (HFE) mature protein, mutant H41D.
XX
KW Human; haemochromatosis; HFE; hereditary haemochromatosis;
KW iron overload disease; iron deficiency disease; Beta2-microglobulin;
KW Beta2m; transferrin receptor; anaemia; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 41
FT /note= "Wild-type His substituted by Asp"
XX
PN US6391852-B1.
XX
PD 21-MAY-2002.
XX
PF 12-JUN-1998; 98US-00094964.
XX
PR 13-JUN-1997; 97US-00876010.
XX
PA (BIRA) BIO-RAD LAB INC.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Feder JN, Bjorkman PJ, Schatzman RC;
XX
DR WPI; 2003-155377/15.
XX
PT Method of treating an iron overload disease comprises administration of a
PT soluble complex comprising a 276 amino acid HFE polypeptide and a full
PT length, wild-type human beta2m.
XX
PS Claim 2; Col 2; 17pp; English.
XX
CC The invention relates to a method of treating an iron overload disease

CC comprising administration of a soluble complex comprising a 276 amino
CC acid mature HFE (hereditary haemochromatosis gene protein) polypeptide
CC (ABG72685-ABG72687) and a full length, wild-type human beta2m (beta2-
CC microglobulin). In a HeLa cell based assay, binding and uptake of ^1^2^5I
CC -transferrin in the presence of purified H63D-HFE/beta2m heterodimers was
CC determined. At a concentration of 250 nM H63D-HFE/ beta2m heterodimers,
CC the transferrin receptor (TfR) displayed a KD for transferrin of 28 nM.
CC At the same concentration of normal HFE/beta_2m heterodimers, TfR
CC displayed a KD for transferrin of 40 nM. In the absence of any
CC HFE/beta_2m heterodimers, TfR displayed a KD for transferrin of 7nM. It
CC was observed that H63D-HFE/beta_2m heterodimers were 30-40 % less
CC efficient in decreasing TfR affinity for transferrin compared to wild-
CC type HFE. The method is useful for treating iron overload diseases and
CC iron deficiency e.g. anaemia. The present sequence is the H63D (residue
CC 63 of the full length protein, 41 of the mature form) mutant from of
CC mature HFE used to investigate the role of the His residue in transferrin
CC receptor binding to transferrin
XX
SQ Sequence 276 AA;

Query Match 98.6%; Score 1493; DB 6; Length 276;
Best Local Similarity 98.9%; Pred. No. 3.4e-129;
Matches 273; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
```

RESULT 12
ABU62093
ID ABU62093 standard; protein; 276 AA.
XX
AC ABU62093;
XX
DT 01-OCT-2003 (first entry)
XX
DE HFE mutant polypeptide #2 useful for treating iron diseases.
XX
KW Iron overload disease; iron deficiency disease; HFE polypeptide;
KW beta2 microglobulin; beta2m; hereditary haemochromatosis; HH; anaemia;
KW protein replacement therapy; defective HFE gene; human; antianaemic;
KW mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2003073627-A1.
XX
PD 17-APR-2003.
XX
PF 04-MAR-2002; 2002US-00092404.
XX
PR 13-JUN-1997; 97US-00876010.
PR 12-JUN-1998; 98US-00094964.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Feder JN, Bjorkman PJ, Schatzman RC;
XX
DR WPI; 2003-567313/53.
XX
PT Treating an iron overload disease (e.g. hemochromatosis) or an iron
PT deficiency disease (e.g. anemia), comprises administering to a patient an
PT HFE polypeptide and full-length, wild type human beta-2 microglobulin.
XX
PS Claim 5; Page 1; 14pp; English.
XX
CC The present invention relates to a method for treating iron overload
CC diseases and iron deficiency diseases. The method comprises administering
CC to a patient an HFE polypeptide. The HFE polypeptide is provided in a
CC complex with full-length, wild type human beta2 microglobulin (beta2m).
CC The method and HFE polypeptide are useful for diagnosing or treating an
CC iron overload disease (e.g. hereditary haemochromatosis, HH) or an iron
CC deficiency disease (e.g. anaemia). The HFE polypeptide is also useful in
CC protein replacement therapy for individuals having a defective HFE gene.
CC The present sequence represents an HFE polypeptide useful for treating
CC iron diseases
XX
SQ Sequence 276 AA;

Query Match 98.6%; Score 1493; DB 6; Length 276;
Best Local Similarity 98.9%; Pred. No. 3.4e-129;
Matches 273; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
```

RESULT 13
AAB36871
ID AAB36871 standard; protein; 348 AA.
XX
AC AAB36871;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human hereditary hemochromatosis 24d2 mutation protein.
XX
KW HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload.
XX
OS Homo sapiens.
XX
PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-00834497.
XX
PR 04-APR-1996; 96US-00630912.
PR 16-APR-1996; 96US-00632673.
PR 23-MAY-1996; 96US-00652265.

XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI; 2001-006341/01.
DR N-PSDB; AAC68427.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful for
PT treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload.
XX
PS Claim 3; Fig 4; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene
XX
SQ Sequence 348 AA;

Query Match 98.6%; Score 1493; DB 4; Length 348;
Best Local Similarity 98.9%; Pred. No. 4.5e-129;
Matches 273; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298
```

RESULT 14
AAB36870
ID AAB36870 standard; protein; 348 AA.
XX
AC AAB36870;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human hereditary hemochromatosis 24d1 mutation protein.
XX
KW HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload.
XX
OS Homo sapiens.
XX
PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-00834497.
XX
PR 04-APR-1996; 96US-00630912.
PR 16-APR-1996; 96US-00632673.
PR 23-MAY-1996; 96US-00652265.

XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI; 2001-006341/01.
DR N-PSDB; AAC68426.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful for
PT treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload.
XX
PS Claim 2; Fig 3; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene
XX
SQ Sequence 348 AA;

Query Match 98.5%; Score 1491; DB 4; Length 348;
Best Local Similarity 98.9%; Pred. No. 6.9e-129;
Matches 273; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
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Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||| |||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTYQVEHPGLDQPLIVIWE 298
```

RESULT 15
ABU62092
ID ABU62092 standard; protein; 276 AA.
XX
AC ABU62092;
XX
DT 01-OCT-2003 (first entry)
XX
DE HFE mutant polypeptide #1 useful for treating iron diseases.
XX
KW Iron overload disease; iron deficiency disease; HFE polypeptide;
KW beta2 microglobulin; beta2m; hereditary haemochromatosis; HH; anaemia;
KW protein replacement therapy; defective HFE gene; human; antianaemic;
KW mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2003073627-A1.
XX
PD 17-APR-2003.
XX
PF 04-MAR-2002; 2002US-00092404.
XX

PR 13-JUN-1997; 97US-00876010.
PR 12-JUN-1998; 98US-00094964.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Feder JN, Bjorkman PJ, Schatzman RC;
XX
DR WPI; 2003-567313/53.
XX
PT Treating an iron overload disease (e.g. hemochromatosis) or an iron
PT deficiency disease (e.g. anemia), comprises administering to a patient an
PT HFE polypeptide and full-length, wild type human beta-2 microglobulin.
XX
PS Claim 3; Page 1; 14pp; English.
XX
CC The present invention relates to a method for treating iron overload
CC diseases and iron deficiency diseases. The method comprises administering
CC to a patient an HFE polypeptide. The HFE polypeptide is provided in a
CC complex with full-length, wild type human beta2 microglobulin (beta2m).
CC The method and HFE polypeptide are useful for diagnosing or treating an
CC iron overload disease (e.g. hereditary haemochromatosis, HH) or an iron
CC deficiency disease (e.g. anaemia). The HFE polypeptide is also useful in
CC protein replacement therapy for individuals having a defective HFE gene.
CC The present sequence represents an HFE polypeptide useful for treating
CC iron diseases
XX
SQ Sequence 276 AA;

Query Match 98.2%; Score 1486; DB 6; Length 276;
Best Local Similarity 98.6%; Pred. No. 1.5e-128;
Matches 272; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        181 DQQVPPLVKVTHHVTSSVTTLRCPALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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GenCore version 5.1.6

OM protein - protein search, using sw model

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Searched: 220531 seqs, 31899231 residues

Total number of hits satisfying chosen parameters: 220531

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1502	99.2	348	6	US-10-796-280-895	Sequence 895, App
2	1412	93.3	334	6	US-10-796-280-904	Sequence 904, App
3	1367	90.3	325	6	US-10-796-280-898	Sequence 898, App
4	1366	90.2	280	6	US-10-796-280-901	Sequence 901, App
5	1017	67.2	260	6	US-10-796-280-897	Sequence 897, App
6	942	62.2	256	6	US-10-796-280-900	Sequence 900, App
7	927	61.2	246	6	US-10-796-280-903	Sequence 903, App
8	862	56.9	242	6	US-10-796-280-894	Sequence 894, App
9	652	43.1	161	6	US-10-796-280-899	Sequence 899, App
10	515	34.0	168	6	US-10-796-280-902	Sequence 902, App
11	506	33.4	365	6	US-10-767-471-755	Sequence 755, App
12	504	33.3	415	1	PCT-US04-10531-109	Sequence 109, App
13	503	33.2	365	6	US-10-821-234-1575	Sequence 1575, Ap
14	489.5	32.3	175	6	US-10-796-280-896	Sequence 896, App
15	484	32.0	338	6	US-10-767-471-869	Sequence 869, App
16	484	32.0	338	6	US-10-767-471-873	Sequence 873, App
17	484	32.0	338	6	US-10-821-234-1565	Sequence 1565, Ap
18	484	32.0	343	6	US-10-767-471-874	Sequence 874, App
19	476	31.4	365	6	US-10-767-471-753	Sequence 753, App
20	476	31.4	365	6	US-10-767-471-754	Sequence 754, App
21	476	31.4	365	7	US-60-552-390-257	Sequence 257, App
22	476	31.4	365	7	US-60-552-390-258	Sequence 258, App
23	472	31.2	362	6	US-10-767-471-951	Sequence 951, App
24	472	31.2	362	6	US-10-767-471-952	Sequence 952, App
25	472	31.2	362	7	US-60-552-390-260	Sequence 260, App
26	472	31.2	362	7	US-60-552-390-264	Sequence 264, App
27	467	30.8	331	6	US-10-767-471-953	Sequence 953, App
28	467	30.8	331	7	US-60-552-390-263	Sequence 263, App
29	467	30.8	366	6	US-10-767-471-959	Sequence 959, App
30	464	30.6	366	6	US-10-767-471-955	Sequence 955, App
31	464	30.6	366	6	US-10-767-471-958	Sequence 958, App
32	464	30.6	366	7	US-60-552-390-259	Sequence 259, App
33	464	30.6	366	7	US-60-552-390-262	Sequence 262, App
34	464	30.6	442	6	US-10-767-471-1135	Sequence 1135, Ap
35	464	30.6	703	6	US-10-767-471-956	Sequence 956, App
36	464	30.6	703	7	US-60-552-390-261	Sequence 261, App
37	463	30.6	362	6	US-10-767-471-684	Sequence 684, App
38	461	30.4	365	1	PCT-US02-39555A-1047	Sequence 1047, Ap
39	461	30.4	365	6	US-10-128-558-136	Sequence 136, App
40	460	30.4	362	7	US-60-552-390-265	Sequence 265, App
41	458	30.3	406	6	US-10-767-471-685	Sequence 685, App
42	457	30.2	362	6	US-10-767-471-954	Sequence 954, App
43	457	30.2	362	6	US-10-767-471-957	Sequence 957, App
44	457	30.2	362	7	US-60-552-390-266	Sequence 266, App
45	456	30.1	362	6	US-10-767-471-1136	Sequence 1136, Ap

ALIGNMENTS

RESULT 1
US-10-796-280-895
; Sequence 895, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; CURRENT APPLICATION NUMBER: US/10/796,280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 895
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-796-280-895

Query Match 99.2%; Score 1502; DB 6; Length 348;
Best Local Similarity 99.3%; Pred. No. 8e-116;
Matches 274; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298
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RESULT 2
US-10-796-280-904
; Sequence 904, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

```
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001510
;  CURRENT APPLICATION NUMBER: US/10/796,280
;  CURRENT FILING DATE:  2004-03-10
;  NUMBER OF SEQ ID NOS: 68533
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 904
;   LENGTH: 334
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-796-280-904

  Query Match            93.3%;  Score 1412;  DB 6;  Length 334;
  Best Local Similarity   94.2%;  Pred. No. 1.8e-108;
  Matches  260;  Conservative    0;  Mismatches    2;  Indels   14;  Gaps    1;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              |||                |||||||||||||||||||||||||||||||||||||||||
Db        203 DQQ--------------VTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 248

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||||||||||||||||||||
Db        249 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 284


RESULT 3
US-10-796-280-898
; Sequence 898, Application US/10796280
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001510
;  CURRENT APPLICATION NUMBER: US/10/796,280
;  CURRENT FILING DATE:  2004-03-10
;  NUMBER OF SEQ ID NOS: 68533
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 898
;   LENGTH: 325
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-796-280-898

  Query Match            90.3%;  Score 1367;  DB 6;  Length 325;
  Best Local Similarity   99.2%;  Pred. No. 8.7e-105;
  Matches  247;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         28 LGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQLSQSLKGWDHMFTVDFWTIMENH 87
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 LGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQLSQSLKGWDHMFTVDFWTIMENH 86

Qy         88 NASKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDALEFCPDTLDWRAAEPRAWPTKLEW 147
              | ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db         87 NHSKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDHLEFCPDTLDWRAAEPRAWPTKLEW 146

Qy        148 ERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQVPPLVKVTHHVTSSVTTLRCRALN 207
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 ERHKIRARQNRAYLERDCPAQLQQLLELGRGVLDQQVPPLVKVTHHVTSSVTTLRCRALN 206

Qy        208 YYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGL 267
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 YYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGL 266

Qy        268 DQPLIVIWE 276
              |||||||||
Db        267 DQPLIVIWE 275


RESULT 4
US-10-796-280-901
; Sequence 901, Application US/10796280
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001510
;  CURRENT APPLICATION NUMBER: US/10/796,280
;  CURRENT FILING DATE:  2004-03-10
;  NUMBER OF SEQ ID NOS: 68533
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 901
;   LENGTH: 280
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-796-280-901

  Query Match            90.2%;  Score 1366;  DB 6;  Length 280;
  Best Local Similarity   99.2%;  Pred. No. 8.8e-105;
  Matches  250;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPP 252
              ||||||||||||
Db        263 TYQGWITLAVPP 274


RESULT 5
US-10-796-280-897
; Sequence 897, Application US/10796280
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001510
;  CURRENT APPLICATION NUMBER: US/10/796,280
;  CURRENT FILING DATE:  2004-03-10
;  NUMBER OF SEQ ID NOS: 68533
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 897
;   LENGTH: 260
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-796-280-897

  Query Match            67.2%;  Score 1017;  DB 6;  Length 260;
  Best Local Similarity   98.9%;  Pred. No. 3.4e-76;
  Matches  183;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         92 ESHTLQVILGCEMQEDNSTEGYWKYGYDGQDALEFCPDTLDWRAAEPRAWPTKLEWERHK 151
```

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                :|||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          26 QSHTLQVILGCEMQEDNSTEGYWKYGYDGQDHLEFCPDTLDWRAAEPRAWPTKLEWERHK 85

Qy         152 IRARQNRAYLERDCPAQLQQLLELGRGVLDQQVPPLVKVTHHVTSSVTTLRCRALNYYPQ 211
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          86 IRARQNRAYLERDCPAQLQQLLELGRGVLDQQVPPLVKVTHHVTSSVTTLRCRALNYYPQ 145

Qy         212 NITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPL 271
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         146 NITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPL 205

Qy         272 IVIWE 276
               |||||
Db         206 IVIWE 210


RESULT 6
US-10-796-280-900
; Sequence 900, Application US/10796280
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001510
;  CURRENT APPLICATION NUMBER: US/10/796,280
;  CURRENT FILING DATE:  2004-03-10
;  NUMBER OF SEQ ID NOS: 68533
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 900
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-796-280-900

  Query Match             62.2%;  Score 942;  DB 6;  Length 256;
  Best Local Similarity   66.3%;  Pred. No. 4.7e-70;
  Matches  183;  Conservative    0;  Mismatches    1;  Indels   92;  Gaps    1;

Qy           1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy          61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
               |||||||||||||||||||||||||| ||
Db          83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSK---------------------------- 113

Qy         121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

Db         114 ------------------------------------------------------------ 113

Qy         181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         114 ---VPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 170

Qy         241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
               |||||||||||||||||||||||||||||||||||
Db         171 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 206


RESULT 7
US-10-796-280-903
; Sequence 903, Application US/10796280
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001510
;  CURRENT APPLICATION NUMBER: US/10/796,280
;  CURRENT FILING DATE:  2004-03-10
;  NUMBER OF SEQ ID NOS: 68533
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 903
;   LENGTH: 246
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-796-280-903

  Query Match             61.2%;  Score 927;  DB 6;  Length 246;
  Best Local Similarity   91.4%;  Pred. No. 7.6e-69;
  Matches  169;  Conservative    1;  Mismatches    1;  Indels   14;  Gaps    1;

Qy          92 ESHTLQVILGCEMQEDNSTEGYWKYGYDGQDALEFCPDTLDWRAAEPRAWPTKLEWERHK 151
               :|||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          26 QSHTLQVILGCEMQEDNSTEGYWKYGYDGQDHLEFCPDTLDWRAAEPRAWPTKLEWERHK 85

Qy         152 IRARQNRAYLERDCPAQLQQLLELGRGVLDQQVPPLVKVTHHVTSSVTTLRCRALNYYPQ 211
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          86 IRARQNRAYLERDCPAQLQQLLELGRGVLDQQ--------------VTTLRCRALNYYPQ 131

Qy         212 NITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPL 271
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         132 NITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPL 191

Qy         272 IVIWE 276
               |||||
Db         192 IVIWE 196


RESULT 8
US-10-796-280-894
; Sequence 894, Application US/10796280
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001510
;  CURRENT APPLICATION NUMBER: US/10/796,280
;  CURRENT FILING DATE:  2004-03-10
;  NUMBER OF SEQ ID NOS: 68533
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 894
;   LENGTH: 242
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-796-280-894

  Query Match             56.9%;  Score 862;  DB 6;  Length 242;
  Best Local Similarity   61.2%;  Pred. No. 1.6e-63;
  Matches  169;  Conservative    0;  Mismatches    1;  Indels  106;  Gaps    1;

Qy           1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy          61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
               |||||||||||||||||||||||||| ||
Db          83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSK---------------------------- 113

Qy         121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

Db         114 ------------------------------------------------------------ 113

Qy         181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
                           ||||||||||||||||||||||||||||||||||||||||||||||||
Db         114 -----------------VTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 156

Qy         241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
               |||||||||||||||||||||||||||||||||||
Db         157 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 192


RESULT 9
US-10-796-280-899
; Sequence 899, Application US/10796280
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
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;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001510
;  CURRENT APPLICATION NUMBER: US/10/796,280
;  CURRENT FILING DATE:  2004-03-10
;  NUMBER OF SEQ ID NOS: 68533
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 899
;   LENGTH: 161
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-796-280-899

  Query Match             43.1%;  Score 652;  DB 6;  Length 161;
  Best Local Similarity   99.2%;  Pred. No. 1.7e-46;
  Matches  120;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 Q 121
              |
Db        143 Q 143


RESULT 10
US-10-796-280-902
; Sequence 902, Application US/10796280
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001510
;  CURRENT APPLICATION NUMBER: US/10/796,280
;  CURRENT FILING DATE:  2004-03-10
;  NUMBER OF SEQ ID NOS: 68533
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 902
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-796-280-902

  Query Match             34.0%;  Score 515;  DB 6;  Length 168;
  Best Local Similarity   89.8%;  Pred. No. 3e-35;
  Matches   97;  Conservative    2;  Mismatches    5;  Indels    4;  Gaps    1;

Qy        169 LQQLLELGRGVLDQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKE 228
              ||  :  || :|    ||||||||||||||||||||||||||||||||||||||||||||
Db         15 LQTAVLQGRLLL----PPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKE 70

Qy        229 FEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 FEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 118


RESULT 11
US-10-767-471-755
; Sequence 755, Application US/10767471
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001505
;  CURRENT APPLICATION NUMBER: US/10/767,471
;  CURRENT FILING DATE:  2004-01-30
;  NUMBER OF SEQ ID NOS: 50231
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 755
;   LENGTH: 365
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-767-471-755

  Query Match             33.4%;  Score 506;  DB 6;  Length 365;
  Best Local Similarity   39.6%;  Pred. No. 4.1e-34;
  Matches  110;  Conservative   46;  Mismatches  112;  Indels   10;  Gaps    8;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |    |   | |:|||||  || :| :  |:|:||| ||:      : |
Db         26 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
                | ::::|       ||  |:   :| |:  |||:|:: ||::  |     || :  |||
Db         85 DQETRNVKAQSQTDRVDLGTLRGYYNQSEAGSHTIQIMYGCDVGSDGRFLRGYRQDAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWE-RHKIRARQNRAYLERDCPAQLQQLLELGRGV 179
              :| :    |   | ||:  |  || :||  |:  | | ||||:  |   |:: || |:
Db        145 KDYIALNEDLRSWTAADMAAQITKRKWEAAHE--AEQLRAYLDGTCVEWLRRYLENGKET 202

Qy        180 LDQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNG 238
              | :  ||   :||| ::    |||| || :||  ||: | :| :    :: |  :  | |
Db        203 LQRTDPPKTHMTHHPISDHEATLRCWALGFYPAEITLTWQRDGED-QTQDTELVETRPAG 261

Qy        239 DGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||:| |  : || |||||||| |:| || :|| : ||
Db        262 DGTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWE 299


RESULT 12
PCT-US04-10531-109
; Sequence 109, Application PC/TUS0410531
; GENERAL INFORMATION:
;  APPLICANT: diaDexus, Inc.
;  APPLICANT:  Macina, Roberto
;  APPLICANT:  Turner, Leah R
;  APPLICANT:  Sun, Yongming
;  TITLE OF INVENTION: Compositions, Splice Variants and Methods Relating to Colon Spec
;  TITLE OF INVENTION:  Genes and Proteins
;  FILE REFERENCE: DEX-0476
;  CURRENT APPLICATION NUMBER: PCT/US04/10531
;  CURRENT FILING DATE:  2004-04-09
;  PRIOR APPLICATION NUMBER: US 06/460,711
;  PRIOR FILING DATE: 2003-04-02
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
;   LENGTH: 415
;   TYPE: PRT
;   ORGANISM: Homo sapien
PCT-US04-10531-109

  Query Match             33.3%;  Score 504;  DB 1;  Length 415;
  Best Local Similarity   39.0%;  Pred. No. 6.9e-34;
  Matches  108;  Conservative   48;  Mismatches  113;  Indels    8;  Gaps    7;

Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |    |   | |:|||||  || :| :  |:|:||| ||:      : |
Db         76 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 134

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
                : ::::|       ||  |:   :| |:  |||:|:: ||::  |     || :  |||
Db        135 DRETRNVKAHSQTDRVDLGTLRGYYNQSEAGSHTIQMMYGCDVGSDGRFLRGYQQDAYDG 194

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| :    |   | ||:  |  || :||  :  | | |||||  |   |:: || |:  |
Db        195 KDYIALNEDLRSWTAADMAAQITKRKWEAAHV-AEQLRAYLEGTCVEWLRRYLENGKETL 253

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :  ||   :||| ::    |||| ||:: ||: | :| :    :: |  :  | ||
Db        254 QRTDPPKTHMTHHPISDHEATLRCWALSFYPAEITLTWQRDGED-QTQDTELVETRPAGD 312
```

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Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |:|||||| |:| || :|| : ||
Db        313 GTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRWE 349
```

RESULT 13
US-10-821-234-1575
; Sequence 1575, Application US/10821234
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1575
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1575

Query Match 33.2%; Score 503; DB 6; Length 365;
Best Local Similarity 39.4%; Pred. No. 7.2e-34;
Matches 109; Conservative 44; Mismatches 116; Indels 8; Gaps 7;

```
Qy          5 SHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHE--SRRVEPRTPWVSSRISSQMW 62
              |||: | |   |   |   | |:|||||  || :| :  |:|:||| ||:      : |
Db         26 SHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQE-GPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASKE-SHTLQVILGCEMQED-NSTEGYWKYGYDG 120
                :: :|      || |:   :| |:  |||:| : ||::  |     || :| |||
Db         85 DGETRKVKAHSQTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDVGSDWRFLRGYHQYAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| :   |  | ||:  |  || :||   : | | |||||  |   |:: || |:  |
Db        145 KDYIALKEDLRSWTAADMAAQTTKHKWEAAHV-AEQQRAYLEGTCVEWLRRYLENGKETL 203

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :  |  :||| |:    |||| ||::||  ||: | :| :    :: | :  | ||
Db        204 QRTDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGED-QTQDTELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||:| |  : || |:|||||| |:| || :|| : ||
Db        263 GTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRWE 299
```

RESULT 14
US-10-796-280-896
; Sequence 896, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; CURRENT APPLICATION NUMBER: US/10/796,280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 896
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-796-280-896

Query Match 32.3%; Score 489.5; DB 6; Length 175;
Best Local Similarity 71.1%; Pred. No. 3.9e-33;
Matches 96; Conservative 4; Mismatches 10; Indels 25; Gaps 1;

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Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
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Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILG------------------- 101
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Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKEGSESSSLPGKGKQIPSPHPSSFLSSASF 142

Qy        102 ------CEMQEDNST 110
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Db        143 GEGDTSCDLFSDHST 157
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RESULT 15
US-10-767-471-869
; Sequence 869, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 869
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-767-471-869

Query Match 32.0%; Score 484; DB 6; Length 338;
Best Local Similarity 39.0%; Pred. No. 2.4e-32;
Matches 108; Conservative 43; Mismatches 118; Indels 8; Gaps 7;

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Db         26 SHSMRYFSAAVSRPGRGEPRFIAMGYVDDTQFVRFDSDSACPRMEPRAPWVEQE-GPEYW 84

Qy         63 LQLSQSLKGWDHMFTVDFWTIMENHNASK-ESHTLQVILGCEMQEDNS-TEGYWKYGYDG 120
                : ::: |       ::  |:   :| |:  ||||| ::||::  |     || :| |||
Db         85 EEETRNTKAHAQTDRMNLQTLRGYYNQSEASSHTLQWMIGCDLGSDGRLLRGYEQYAYDG 144

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              :| |     | ||:  |  :| :|   : | | |||||  |   | : || |: :|
Db        145 KDYLALNEDLRSWTAADTAAQISKRKCEAANV-AEQRRAYLEGTCVEWLHRYLENGKEML 203

Qy        181 DQQVPPLVKVTHH-VTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGD 239
              :  ||   |||| |     |||| || :||  | : | :| :    :: |  :  | ||
Db        204 QRADPPKTHVTHHPVFDYEATLRCWALGFYPAEIILTWQRDGED-QTQDVELVETRPAGD 262

Qy        240 GTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        263 GTFQKWAAVVVPSGEEQRYTCHVQHEGLPEPLMLRWK 299
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Search completed: May 4, 2004, 11:48:58
Job time : 11 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 4, 2004, 11:32:18 ; Search time 14.3333 Seconds
(without alignments)
994.100 Million cell updates/sec

Title: US-10-092-404-3
Perfect score: 1514
Sequence: 1 RLLRSHSLHYLFMGASEQDL.....RYTCQVEHPGLDQPLIVIWE 276

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1514	100.0	276	4	US-09-094-964-3	Sequence 3, Appli
2	1502	99.2	276	4	US-09-094-964-1	Sequence 1, Appli
3	1502	99.2	348	3	US-08-652-265-2	Sequence 2, Appli
4	1502	99.2	348	3	US-08-834-497A-2	Sequence 2, Appli
5	1502	99.2	348	3	US-09-503-444A-2	Sequence 2, Appli
6	1502	99.2	348	4	US-09-277-457-2	Sequence 2, Appli
7	1502	99.2	348	4	US-09-679-729-2	Sequence 2, Appli
8	1493	98.6	276	4	US-09-094-964-2	Sequence 2, Appli
9	1493	98.6	348	3	US-08-652-265-6	Sequence 6, Appli
10	1493	98.6	348	3	US-08-834-497A-6	Sequence 6, Appli
11	1493	98.6	348	3	US-09-503-444A-6	Sequence 6, Appli
12	1491	98.5	348	3	US-08-652-265-4	Sequence 4, Appli
13	1491	98.5	348	3	US-08-834-497A-4	Sequence 4, Appli
14	1491	98.5	348	3	US-09-503-444A-4	Sequence 4, Appli
15	1482	97.9	348	3	US-08-652-265-8	Sequence 8, Appli
16	1482	97.9	348	3	US-08-834-497A-8	Sequence 8, Appli
17	1482	97.9	348	3	US-09-503-444A-8	Sequence 8, Appli
18	517	34.1	361	3	US-08-652-265-22	Sequence 22, Appl
19	517	34.1	361	3	US-08-834-497A-22	Sequence 22, Appl
20	517	34.1	361	3	US-09-503-444A-22	Sequence 22, Appl
21	511	33.8	364	4	US-08-914-372C-11	Sequence 11, Appl
22	508	33.6	365	3	US-08-652-265-23	Sequence 23, Appl
23	508	33.6	365	3	US-08-834-497A-23	Sequence 23, Appl
24	508	33.6	365	3	US-09-503-444A-23	Sequence 23, Appl
25	500	33.0	274	2	US-08-484-905-107	Sequence 107, App
26	500	33.0	274	3	US-08-481-985B-107	Sequence 107, App
27	500	33.0	274	3	US-08-370-476-107	Sequence 107, App
28	500	33.0	341	3	US-08-890-719-38	Sequence 38, Appl
29	499	33.0	365	2	US-08-484-905-97	Sequence 97, Appl
30	499	33.0	365	3	US-08-481-985B-97	Sequence 97, Appl
31	499	33.0	365	3	US-08-370-476-97	Sequence 97, Appl
32	498	32.9	274	2	US-08-484-905-108	Sequence 108, App
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34	498	32.9	274	3	US-08-370-476-108	Sequence 108, App
35	498	32.9	365	2	US-08-484-905-100	Sequence 100, App
36	498	32.9	365	3	US-08-481-985B-100	Sequence 100, App
37	498	32.9	365	3	US-08-370-476-100	Sequence 100, App
38	497	32.8	274	1	US-08-222-851-1	Sequence 1, Appli
39	497	32.8	363	4	US-08-914-372C-37	Sequence 37, Appl
40	497	32.8	365	2	US-08-484-905-99	Sequence 99, Appl
41	497	32.8	365	3	US-08-481-985B-99	Sequence 99, Appl
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43	496	32.8	274	2	US-08-484-905-106	Sequence 106, App
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45	496	32.8	274	3	US-08-370-476-106	Sequence 106, App

ALIGNMENTS

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RESULT 1
US-09-094-964-3
; Sequence 3, Application US/09094964
; Patent No. 6391852
;  GENERAL INFORMATION:
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Bjorkman, Pamela J.
;    APPLICANT:  Schatzman, Randall C.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF IRON OVERLOAD DISEASES
;    TITLE OF INVENTION:  AND IRON DEFICIENCY DISEASES
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds, LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/094,964
;      FILING DATE:  June 12, 1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/876,010
;      FILING DATE:  June 13, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0074-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  276 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-094-964-3

  Query Match           100.0%;  Score 1514;  DB 4;  Length 276;
  Best Local Similarity  100.0%;  Pred. No. 8.6e-144;
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Db          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
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Db         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

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Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
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Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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RESULT 2
US-09-094-964-1
; Sequence 1, Application US/09094964
; Patent No. 6391852
;  GENERAL INFORMATION:
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Bjorkman, Pamela J.
;    APPLICANT:  Schatzman, Randall C.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF IRON OVERLOAD DISEASES
;    TITLE OF INVENTION:  AND IRON DEFICIENCY DISEASES
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds, LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/094,964
;      FILING DATE:  June 12, 1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/876,010
;      FILING DATE:  June 13, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0074-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  276 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-094-964-1

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  Best Local Similarity   99.3%;  Pred. No. 1.4e-142;

  Matches  274;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
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Db        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

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RESULT 3
US-08-652-265-2
; Sequence 2, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-265-2

  Query Match             99.2%;  Score 1502;  DB 3;  Length 348;
  Best Local Similarity   99.3%;  Pred. No. 1.9e-142;
  Matches  274;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Qy         181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
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Db         203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy         241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db         263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 4
US-08-834-497A-2
; Sequence 2, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-834-497A-2

  Query Match             99.2%;  Score 1502;  DB 3;  Length 348;
  Best Local Similarity   99.3%;  Pred. No. 1.9e-142;
  Matches  274;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
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Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

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Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
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Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
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Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 5
US-09-503-444A-2
; Sequence 2, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-503-444A-2

  Query Match             99.2%;  Score 1502;  DB 3;  Length 348;
  Best Local Similarity   99.3%;  Pred. No. 1.9e-142;
  Matches  274;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 6
US-09-277-457-2
; Sequence 2, Application US/09277457
; Patent No. 6355425
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg, Barry E.
;  APPLICANT:  Sawada-Hirai, Ritsuko
;  APPLICANT:  Barton, James C.
;  TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
;  FILE REFERENCE: 10653/002001
;  CURRENT APPLICATION NUMBER: US/09/277,457
;  CURRENT FILING DATE:  1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 348
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-277-457-2

  Query Match             99.2%;  Score 1502;  DB 4;  Length 348;
  Best Local Similarity   99.3%;  Pred. No. 1.9e-142;
  Matches  274;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
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Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
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Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 7
US-09-679-729-2
; Sequence 2, Application US/09679729
; Patent No. 6509442
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg, Barry E.
;  APPLICANT:  Sawada-Hirai, Ritsuko
;  APPLICANT:  Barton, James C.
;  TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
;  FILE REFERENCE: 24065-004 DIV
;  CURRENT APPLICATION NUMBER: US/09/679,729
;  CURRENT FILING DATE:  2000-10-04
;  PRIOR APPLICATION NUMBER: 09/277,457
;  PRIOR FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 348
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-679-729-2

  Query Match             99.2%;  Score 1502;  DB 4;  Length 348;
  Best Local Similarity   99.3%;  Pred. No. 1.9e-142;
  Matches  274;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
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Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 8
US-09-094-964-2
; Sequence 2, Application US/09094964
; Patent No. 6391852
;  GENERAL INFORMATION:
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Bjorkman, Pamela J.
;    APPLICANT:  Schatzman, Randall C.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF IRON OVERLOAD DISEASES
;    TITLE OF INVENTION:  AND IRON DEFICIENCY DISEASES
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds, LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
```

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;       COUNTRY:  USA
;       ZIP:  10036-2811
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  Windows
;       SOFTWARE:  FastSEQ for Windows Version 2.0b
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/094,964
;       FILING DATE:  June 12, 1998
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/876,010
;       FILING DATE:  June 13, 1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poissant, Brian M
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  8907-0074-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-493-4935
;       TELEFAX:  650-493-5556
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  276 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-09-094-964-2

  Query Match             98.6%;  Score 1493;  DB 4;  Length 276;
  Best Local Similarity   98.9%;  Pred. No. 1.1e-141;
  Matches  273;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 60

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276


RESULT 9
US-08-652-265-6
; Sequence 6, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-265-6

  Query Match             98.6%;  Score 1493;  DB 3;  Length 348;
  Best Local Similarity   98.9%;  Pred. No. 1.5e-141;
  Matches  273;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
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Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 10
US-08-834-497A-6
; Sequence 6, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
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;       ZIP:  10036-2811
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  Windows 95
;       SOFTWARE:  FastSEQ for Windows Version 2.0b
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/834,497A
;       FILING DATE:  04-APR-1997
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/652,265
;       FILING DATE:  23-MAY-1996
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/632,673
;       FILING DATE:  16-APR-1996
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/630,912
;       FILING DATE:  04-APR-1996
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poissant, Brian M.
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  8907-0056-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-493-4935
;       TELEFAX:  650-493-5556
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  348 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-834-497A-6

  Query Match             98.6%;  Score 1493;  DB 3;  Length 348;
  Best Local Similarity   98.9%;  Pred. No. 1.5e-141;
  Matches  273;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
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Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              ||||||||||||||||||||||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 11
US-09-503-444A-6
; Sequence 6, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-503-444A-6

  Query Match             98.6%;  Score 1493;  DB 3;  Length 348;
  Best Local Similarity   98.9%;  Pred. No. 1.5e-141;
  Matches  273;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
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Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        263 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 298


RESULT 12
US-08-652-265-4
; Sequence 4, Application US/08652265
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```
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-265-4

  Query Match             98.5%;  Score 1491;  DB 3;  Length 348;
  Best Local Similarity   98.9%;  Pred. No. 2.4e-141;
  Matches  273;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
              |||||||||||||||||| ||||||||||||||||
Db        263 TYQGWITLAVPPGEEQRYTYQVEHPGLDQPLIVIWE 298


RESULT 13
US-08-834-497A-4
; Sequence 4, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-834-497A-4

  Query Match             98.5%;  Score 1491;  DB 3;  Length 348;
  Best Local Similarity   98.9%;  Pred. No. 2.4e-141;
  Matches  273;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        263 TYQGWITLAVPPGEEQRYTYQVEHPGLDQPLIVIWE 298


RESULT 14
US-09-503-444A-4
; Sequence 4, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-503-444A-4

  Query Match             98.5%;  Score 1491;  DB 3;  Length 348;
  Best Local Similarity   98.9%;  Pred. No. 2.4e-141;
  Matches  273;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 202

Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 262

Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        263 TYQGWITLAVPPGEEQRYTYQVEHPGLDQPLIVIWE 298


RESULT 15
US-08-652-265-8
; Sequence 8, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  348 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-265-8

  Query Match             97.9%;  Score 1482;  DB 3;  Length 348;
  Best Local Similarity   98.6%;  Pred. No. 1.9e-140;
  Matches  272;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQ 60
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Db         23 RLLRSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDDESRRVEPRTPWVSSRISSQ 82

Qy         61 MWLQLSQSLKGWDHMFTVDFWTIMENHNASKESHTLQVILGCEMQEDNSTEGYWKYGYDG 120
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Db         83 MWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDG 142

Qy        121 QDALEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVL 180
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 DQQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDG 240
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Qy        241 TYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIWE 276
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Db        263 TYQGWITLAVPPGEEQRYTYQVEHPGLDQPLIVIWE 298


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